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Db 462 GCGCTGTACGGCAGCAACCCATCGCGCGCGGTGAGTACTTACCCCTCGACCGCTCG 521
Qy 505 GATTTGCTGTTGGACGACAGGCAATTCGCGGTGATGATGATAAAGCGTTACAGAGCGCG 564
Db 522 GACATCATCAAGACGCGGAGGACGTCGCGCGCCCGCTGAAGCGCGCTTACGAGTCGGCC 581
Qy 565 AACCGCGAATGACAAATACACTCGGTTTCGGTGTGAGCAACGACCGCGTGATGCGGCT 624
Db 582 ACCCACTCTGTTGACCTCGGCCACCGTCGCGCGCGCGCGCACCTTCGACGGGCTG 641
Qy 625 TTGCTGTATTCGACGTCGCGGTGATGAGACCGAAGCGCGCGGAGGCTGCTATCGG 684
Db 642 CTGCATTATGCTACCGCGGAGGCGCACGAGCCGAATCCAACGGCGGCGCACGGGGCAC 701
Qy 685 GTAGAGGGTGTGGCAGCGGA 705
Db 702 CGGGGCTCTTCGGGCAAGNCGA 722

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RESULT 2
BZ558933 1155 bp DNA linear GSS 17-DEC-2002
LOCUS pac82-164_1131.s1 pac82-164 Pseudomonas aeruginosa genomic clone
DEFINITION pac82-164_1131, genomic survey sequence.
ACCESSION BZ558933
VERSION BZ558933.1 GI:27174323
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

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REFERENCE 1 (bases 1 to 1155)
AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

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FEATURES
source
Location/Qualifiers
1..1155
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
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/clone_lib="pac82-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."

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ORIGIN
Query Match 2.7%; Score 63.8; DB 8; Length 1155;
Best Local Similarity 49.7%; Pred. No. 7.2e-08;
Matches 189; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

Qy 268 GCGTTTGTGTCGGCGCGTGAAGCAACCGTGTGTCGTTGATGAGCAATTCGACGCGGTGAGC 327
Db 233 GCGTCGCCCAAGCGGCGGACAGACACCAACATCTGGGGCTGGGGCGACCGCGGAGAC 292
Qy 328 CTGCTGTATTCGGAAGAAACTCAGTGTATGACGTTATGGCAATTCGAACAGCTGCGGC 387
Db 293 GTGCCCTATACCTGTGACGCGCGCAGAGAGCGGCTTCGAGCGCTTACCAGCAGGCGCAC 352
Qy 388 CTGCTCTACGCCCAACTCTGTCGCCAATCGCAATCGGAAGCGCGCTGACTCTTTC 447
Db 353 GTGTTTCATCAACCGGAAATGATCAAGCGCATCGAGGTGGAGAGGACCGCACTCGGTG 412

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Qy 448 AATACCGGTAGCGCGCATTTGGTGGCGCGGTGAATTACAAACCGCTGCAAGGACATGAT 507
Db 413 TTCACCGGCATGGCGGCTTCGGCGGCACCGTGCACATGGAGACCAAGGACGCGCGGAC 472
Qy 508 TTGCTGTTGGACGACGAGCAATTCGCGGTGATGATGAAAAAGCGTTACAGAGCGCGCAAC 567
Db 473 CTGCTGCGGAGGCGCGGACGTCGCGCGCATGCTCAAGTACGGCTATCACTTCCAAACGAC 532
Qy 568 CGCGAATGACAAATACACTCGGT--TTCGGTGTGAGCAACGACCGCGTGATGCGGCT 624
Db 533 CAGCAGAAGATCTACTTCGGCGCTGTGTTGGCGCCACGANNAGACCGCGCGTGCATGCC 592
Qy 625 TTGCTGTATTCGCAACGTCG 644
Db 593 CTGCTCTATCTCAACGGTCG 612

RESULT 3
BZ572005 916 bp DNA linear GSS 17-DEC-2002
LOCUS msh2_225.y1 msh Pseudomonas aeruginosa genomic clone msh2_225,
DEFINITION genomic survey sequence.
ACCESSION BZ572005
VERSION BZ572005.1 GI:27207066
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 916)
AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

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FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="MSH"
/db_xref="taxon:287"
/clone="msh2_225"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library."

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ORIGIN
Query Match 2.7%; Score 63.6; DB 8; Length 916;
Best Local Similarity 50.3%; Pred. No. 7.7e-08;
Matches 184; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

Qy 284 GCGTGAAGGCAACCGTGTGCGTGTGAGCATTCAGCGGTGAGCGTGTGATTCGGAAG 343
Db 504 GCGGCAAGCCACCAACATCTGGGCGCTGGGCGACGCGGAGACGTGCCCTATACCTGG 445
Qy 344 AAACTCACTGTATGACGTTATGCAACTTCAACAGCTCGCGCTGTCTATCGACCGCG 403
Db 444 ACGGCGCGCAAGATTCGGCTTCGAGCGCTACACAGGGGACCGTGTTCATCGAACCG 385
Qy 404 AACTCGTGGCAACATCGAAATTCGGAAGGCGCGCTGACTCTTTTCAATACCGGTAGCGCG 463
Db 384 AAATGATCAAGCGCATCGAGGTGGAGAGGAGCCGCACTCGGTGTTCCACCGCAATGCG 325
Qy 464 CATTGGTGGCGCGGTGAATTACAAACCGTCCAAAGGACATGATTTGCTGTTGGACACA 523

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Result No.	Score	Query Match	Length	DB	ID	Description
1	65.6	2.8	897	8	BZ572021	BZ572021 msh2_233.
2	63.8	2.7	1155	8	BZ558933	BZ558933 pacb2_164
C 3	63.6	2.7	916	8	BZ572005	BZ572005 msh2_225.
C 4	40.2	1.7	493	9	CC624398	CC624398 OGJUS74TV
C 5	40.2	1.7	864	9	CG323747	CG323747 QG2AS83TH
C 6	40	1.7	839	8	BZ553204	BZ553204 pacsl-60
7	39	1.6	704	7	CO435339	CO435339 10a2-t3.M
C 8	38.8	1.6	1101	9	AL077149	AL077149 brosephill
C 9	38.6	1.6	768	7	CF880971	CF880971 tric083xd
10	38.6	1.6	776	8	CB550719	CB550719 pacsl-60
C 11	38.6	1.6	823	6	CB907731	CB907731 tric083xd
C 12	38.6	1.6	830	6	CA767580	CA767580 AF53-Rpf
C 13	38.6	1.6	910	5	BX928168	BX928168 BX928168
C 14	38.4	1.6	439	9	CL883336	CL883336 abf60e12.
C 15	38	1.6	486	2	BB851478	BB851478 BB851478
C 16	38	1.6	2181	3	AK077440	AK077440 Mus muscu
17	37.8	1.6	460	4	BI936731	BI936731 dc35c02.y
18	37.8	1.6	856	8	BZ564907	BZ564907 pacb2-164
C 19	37.6	1.6	513	5	BQ825715	BQ825715 1030129C1
20	37.4	1.6	740	7	CF870398	CF870398 tric022xl
21	37.4	1.6	807	6	CB900579	CB900579 tric022xl
22	37.2	1.6	614	7	CF767164	CF767164 CES003263
C 23	37.2	1.6	718	7	CF881736	CF881736 tric085XO
C 24	37.2	1.6	843	6	CB908388	CB908388 tric085XO

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ATTORNEY/AGENT INFORMATION:
; NAME: No. 6121037nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 94,784-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2373
US-08-537-361E-3

Query Match 77.7%; Score 1848; DB 3; Length 2376;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2053; Conservative 0; Mismatches 320; Indels 3; Gaps 1;

QY 1 ATGAAACCATTTACATGCTTCTTATTCGCGCTGTCGCGAGTATTTTCGGCAATCCG 60
DB 1 ATGAAACCATTTACAAATGCCCCCTATCGCGCGCTGCTCGGCAGTATTTTCGGCAATCCG 60

QY 61 GTCTTGGCAGCGGATGAAGTGAACCGAAACACACCCCGTTAAAGCAGATAAAGAA 120
DB 61 GTCTTGGCAGATGAAGTGAACCGAAACACACCCCGTTAAAGCAGATGAAGAA 120

QY 121 GTGCGGTAAAGACACAGCTTAAATGCGCTGCAACCGTGAACCTGTCAACCTCGGCGC 180
DB 121 GTGCGGTAAAGACACAGCTTAAATGCGCTGCAACCGTGAACCTGTCAACCTCGGCGC 180

QY 181 ATTCAACAGGAATGATACGCGACACAAAGACTTGTGCGTACTCCACCGAGTCGCG 240
DB 181 ATCAACAGGAATGATACGCGACCAATAAGACTTGTGCGCTATTCACCGAGTTCGCG 240

QY 241 TTGAGCGATAGCGCGCCATCAAAAGGCTTTCTGTGCGCGCGTGAAGGCAACCGT 300
DB 241 TTGAGCGAGGAGCGCGCTCATCAAAAGGCTTTTCCCATTCGCGCGTGAAGGCGAGCGT 300

QY 301 GTGCGGTGACATTTGACGCGGTGAGCTGCTGCTGATTCGGAAGAAACTCACTGTATGCA 360
DB 301 GTGCGGTGATGATGACGCGGTAAACCTGCTGATTCGGAAGAAACTCGCTGTATGCGC 360

QY 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTATATCGACCCCGAACTCGTGCACCAATC 420
DB 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTATATCGACCCCGAACTCGTGCACCAATC 420

QY 421 GAAATCGGAGGCGCTGACTTTCAATACCGGTAGCGCGCATTTGGGTGGCGCGGTG 480
DB 421 GAAATCGGAGGCGCGGACTCTTTCAATACCGCGAGCGCGCTTTGGGCGCGGTG 480

QY 481 AATTACCAACCCCTGCAAGGACATGATTTGCTGTTGACGACAGCGCAATTCGGCGTATG 540
DB 481 AATTACCAACCCCTGCAAGGACGATGACTTACTGTTGCTGAAACCGGAGTTTCGGGTG 540

QY 541 ATGAAAAACCGTTACAGACCGCAACCGGAATGGAACAAATATACCTCGGTTTCGGTGTG 600
DB 541 ATGAAAAACCGTTACAGACCGCAACCGTGAATGGAACAAATATACCTCGGTTTCGGGTG 600

QY 601 AGCAACGACCGGTGATGCGCGCTTGTCTGTTTCGCAACGCTCGCGGTATGACACCGAA 660
DB 601 AGCAACGACCGGTGATGCGCGCTTGTCTGTTTCGCAACGCGCGGTATGAAACTGAA 660

QY 661 AGCGGCGGAGCGGTGATTCGCGGTAGAGGCTGTGCGACGAGCAATATATCCGTGGT 720
DB 661 AGCGGCGGAGCGGTGATTCGCGGTAGAGGCTGTGCGACGAGCAATATATCCGTGGT 720

QY 721 TCCTGACGCGGTATCCCTGATCCGTGCAAAACCAAAATACCAAACTTCTTGGGTAAAGATT 780
DB 721 TCCTGACGCGGTATCCCTGATCCGTGCAAAACCAAAATACCAAACTTCTTGGGTAAAGATT 780

721 TCTGCGCGCGGTATTCCTGATCCGTCCCAACACAAATACCAAGCTTCTTGGGTAAAGATT 780
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901 GTCAACAGAGCGCGTAAACCAACCTTTTACGAATGAGCGCGAATCCGACCGGTG 960
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1021 GGTTCTGTTCCGAGCAATTAACCCACATGGGAAACCGAGTACCATAAAAGGAAGTTGGC 1080
1081 AATATATACAAACCGCAGCATGGACACCCGATTCAAACGTTTACTTTTGGGTATGACAGC 1140
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1258 ACAGCTCGATTCAACCCCGGTGAACCACTAATATATGTTTCTCAGCTGTGTGATCAA 1317
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1318 ATCCATGGAACGACGCTTTCAGCGCGTGAAGATATCGTTACGATCATACCAAAATG 1377
1321 ATCCATGGAACGACGCTTTCAGTAGCGCGAGGATATCGTTACGACCAACCAAAATG 1380
1378 ACCTCTCAGGAATTTGAATGCGAGTGTCTGTTGACAAAAACACCCCTGCGAGCAAT 1437
1381 ACCTCTCAGGAATTTGAATGCGAGTGTCTGTTGACAAAAACACCCCTGCGAGCAAC 1440
1438 ACTTAAAGCGTGGAGCGGATTTGCGGTTTGGCGCGCAACTGATATCAGGCTTGCAT 1497
1441 ACTTAAAGCGTGGAGCGGATTTGCGGTTTGGCGCGCAGCTGAGCCAAACATGCGGT 1500
1498 GTGCGTTTACGACATTTACTTCCGCTACCGTGTCCCAATGCTCCGAGGTGATTTTCACT 1557
1501 TTGGTTTACGATGACCTCAGGTTTCCGCTGCGGATGCGGCTGAGTGTATTTCACT 1560
1558 TACAACACCGTTTGGGTAAATGCGTCCCAATCCCAACCTGAAAGCGAGCGCAGCAC 1617
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1618 ACCCACACCTGCTCTGCAAGGCGCGGAGGAGTACTTTGGATGCCCACTGTAT 1677
1621 ACCCACACCTGCTCTTGCAGGGGCGCGGAGGAGACCTGAGTGGCAACCTGTAT 1680
1678 CAAAACAAATTTACCGCAACTTCTTGTCTGAAGAGCAGAAAGTCTGACACAGCGCGATGTC 1737
1681 CAAAGCAATTTACGAAACTTCTGTCGGAAGAGCAGAAATCTGACTGTGAGCGGACACCC 1740
1738 GGCTGTACTCAGATGAATTTACTACTCGGTATGTGTAGCAATCTTATTCGAAAAACCG 1797
1741 GGCTGTACTGAGGAGGATGCTTACTATATAGATGACGACCCCTACTAAAAAGAACTG 1800
1798 GAATGGCAGATGCAAAATATCGAAGCGCGGATCCGTGCTTGTAGCTGTGACAGCGGT 1857
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Qy	661	AGCGGGCGAGCGTGGCTATCCGGTAGAGGGTCTGGCAGCGAGCAATATATCCGTGGT	720
Db	661	AGCGGGCGAGCGTGGTATATCCGGTAGAGGGTCTGGTAGCGGAGGGAATATCCGTGGT	720
Qy	721	TCGTCAGCGGTATCCCTGATCCGTCCAAACACAAATACGACAACTTCTTGGGTAAAGATT	780
Db	721	TCTCGGCGGGTATTCCTGATCCGTCCCAACAAATACCAAGTCTTCTTGGGTAAAGATT	780
Qy	781	GCTTATCAAATCAACGACCAACCGCATCGCGCATCGCTCAACGCTCAGCAGGGGCAT	840
Db	781	GCTTATCAAATCAACGACCAACCGCATCGCGCATCGCTCAACGCTCAGCAGGGGCAT	840
Qy	841	AATTACAGATTGAAGAGTCTTATAA CCTGACCGGTTCTTCTGGCGGGAAGCCGATGAC	900
Db	841	AATTACAGCGTTGAAGAGTCTTATAA CCGTCTTCTTATTTGGCGTGAAGCTGACGAT	900
Qy	901	GTAACAGACGGCGCAATGCCAACTCTTTTACGAATGGAGCGCTGATTCAAATTTGGCTG	960
Db	901	GTCACAGACGGCGTACACCAACTCTTTTACGAATGGAGCGCGGAATCCGACCGGTG	960
Qy	961	TCGTCCTTTGAAGGGCGAATTTCGATTTATCAGACAAACCAAAGTGGCGGGTTAA CAA CAAA	1020
Db	961	TCTATGTTAAAGCGGATGTCGATTTACAAAACCAAGTATCTGGTCTCACTACAAA	1020
Qy	1021	GGCTCGTTCCGACGGAATATTCACCTGGACGGCAACTATATACGAAGGATTTGGAG	1080
Db	1021	GGTTCGTTCCGACGGAATTA CACCACATGGAAACCGAGTACCAATAAAAGGAAGTTGGC	1080
Qy	1081	AATATATACACCGCAGCAGTGGACACCGGATTCAAA GTTTTACTTTTCGGTATGGACAGC	1140
Db	1081	GAAATCTATACCGCAGCATGGATACAA CCTTTCAAACGATATACGCTGCGTATGGACAGC	1140
Qy	1141	CAACCGTTGCAACT --- GGGCGGCGCAACATCGCTGTTCGCTTAAACCTTTCCGCCAGTCCG	1197
Db	1141	CATCGTTGCAACTCGGGGGGGGGGACACGGCTCTCGTTTAAACCTTTGCGGGCAG	1200
Qy	1198	CGTGAGTTGAAAACCTTAACCGCGACGATTTATCTTCAGCGAGAAAGATATCCCGTACT	1257
Db	1201	CGTGATTTGAAAACCTTAACCGCGACGATTTACTTACTTCAGCGGCGCGTGTGTTCGAACC	1260
Qy	1258	ACCAGCTCGATTCAACACCCCGTGAAACCACTAATTTATGGTTTCTCACTGTCTGATCAA	1317
Db	1261	ACCAACAGTATCCAGCATCCGGTGAAACCA CCAACTACGGTTTCTCGCTGTCCGACCAA	1320
Qy	1318	ATCCAAATGGAACGACGTGTTTCAGCAGCGCTGCAGATATCCGTTACGATCATACCAAAATG	1377
Db	1321	ATCCAAATGGAACGACGTGTTTCAGTAGCGCGCAGGATTCGTTACGACCAACCAAAATG	1380
Qy	1378	ACGCTCAGGAATTTGAATGCGAGTGTATCTGTTGACAAAA CACCGCTGCAGCCAAAT	1437
Db	1381	ACGCTCAGGAATTTGAATGCGACTGT CATGCTTGTGACAAAA CACCGCTGCAGCCAAAC	1440
Qy	1438	ACTTATAAGGCTGGAGGGAATTTGTTCGGTTTGGCGGGCAACTGATATCAGGCTTGCGCAT	1497
Db	1441	ACTTATAAGGCTGGAGCGGAATTTGTTCGGCTTGGCGGCGAGCTGAGCCAAACATGCGCT	1500
Qy	1498	GTCGGTTACGACATTTACTTCGGGCTACGCTGTCCCAATCGCTCCGAAGTGATTTTCACT	1557
Db	1501	GTGGGTTACGATGTGACCTCAGGTTTCGCGTGC CGAATGGGCTGAAGTGATTTTCACT	1560
Qy	1558	TACAACACCGTTCCGGTAAATTTGGCTGCCAATCCCAACTGAAAGCCGAGCGCAGCACCC	1617
Db	1561	TACAACACCGTTCCGGGCATTTGGAAGCCCTAATCCTTAATTTGAAGGCAGAACGCAGCACCC	1620
Qy	1618	ACCCACACCCCTGCTCTGCAAGGCGCGAGCAAAAAGGTACTTTTGGATGCGAACCTGTAT	1677
Db	1621	ACCCACACCCCTGCTCTTGCAGGGGCGGGGACAAAAGGGA CACTGGATGCGCAACTGTAT	1680
Qy	1678	CAAAACAATTACCGCAACTTCTCTCTGTAAGAGCAGAAGCTGACCA CCGCGCGGATGTC	1737
Db	1681	CAAAAGCAATTACCGAAACTTCTCTCTCGAAGAGCAGAAATCTGACTGTCA GCGGCACACC	1740
Qy	1738	GGCTGTACTCAGATGAATTA CTA CCGGTATGTGTAGCAATCTCTTAATTCGAAAAACCG	1797

Db	1741	GGCTGTACTAGGAGGATGCTTACTATATAGATGCAGCGACCCCTACAAAGAAAAAATCTG	1800
Qy	1798	GAATGGCAGATGCAAAATATTCGATAAGGCGCCGAATCCGTGGTCTTGAGCTGCAGAGCCCGT	1857
Db	1801	GATTGGCAGATGAAATAATTCGACAGGCCAGAAATCCGCGATTCGAGTTGACAGGCCCGT	1860
Qy	1858	CTGAATGTGCACAAAAGTAGCGTCTTTTGTTCCTGAGGGCTGGAAATTTGTTCCGCTCGCTG	1917
Db	1861	CTGAATGTGCACAAAAGTAGCGTCTTTTGTTCCTGAGGGTTGAAACTGTTCGCTCGCTG	1920
Qy	1918	GGTTATGCGAAAAGCAAACTGTGCGGGCACAACAGCCTGCTGTCCACACAGCGCCGCAAA	1977
Db	1921	GGTTATGCGAAAAGCAAACTGTGCGGGCACAACAGCCTGCTGTCCACACAGCGCCGCTGAAA	1980
Qy	1978	GTGAATCCCGGTGTGCAGTACGAAAGCCCGAGCGAAAAATGGGGTGTGTTCTCCCGCTG	2037
Db	1981	GTGAATCCCGGTGTGCAGTATGAAGTCCGAGCGAAAAATGGGGCGTATTCTCCCGCTG	2040
Qy	2038	ACTTATCTGGGTGCGAAAAAGGCCAAAGACGCGCAATACACCGTTTATGAAAAACAAGGCG	2097
Db	2041	ACCTATCTAGCGCGAAAAAGGTCAAGACGCGCAATACACCGTTTATGAAAAACAAGGCG	2100
Qy	2098	CGGGGTACGCTTTGCAGAAAAAGTTAAAGATTACCCGTGGCTGAACAAGTCGGCTTAT	2157
Db	2101	TGGGGTACGCTTTGCAGAAAAAGTTAAAGATTACCCGTGGCTGAACAAGTCGGCTTAT	2160
Qy	2158	GTGTTTGATATGTACGGCTTCTACAACTGGCTTAAAAAACCCTGACTTTGCGTGCAGGCGTA	2217
Db	2161	GTGTTTGATATGTACGGCTTCTACAAACC GGCTTAAAAAACCCTGACTTTGCGTGCAGGCGTG	2220
Qy	2218	TATAATGTGTTCAACCGCAATACACACTTGGGATTCCTCGCGCGTTTGTATAGCTAC	2277
Db	2221	TACAACTGTTCAACCGCAATACACACTTGGATTCCTCGCGGTTTATATAGCTAC	2280
Qy	2278	AGCACACCAACCGGGTCGACCGAGATGGCAAGGCTTAGACCGCTACCGCGCTCAGGC	2337
Db	2281	AGCACCAACCAATCGGTCGACCGCGATGGCAAGGCTTAGACCGCTACCGCGGCCAGGC	2340
Qy	2338	CGTAATTACGCCGTATCGCTGGATTTGAACTTTTGA	2373
Db	2341	CGCAATTACGCCGTATCGCTGGAAATGGAATTTTAA	2376
RESULT 10			
US-08-537-361E-3			
; Sequence 3, Application US/08537361E			
; Patent No. 6121037			
; GENERAL INFORMATION:			
; APPLICANT: Stojiljkovic, Igor			
; APPLICANT: So, Magdalene			
; APPLICANT: Hwa, Vivian			
; APPLICANT: Heffron, Fred			
; APPLICANT: Nabsif, Xavier			
; TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor			
; TITLE OF INVENTION: Genes and Uses			
; NUMBER OF SEQUENCES: 14			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff			
; STREET: 300 South Wacker Drive, 32nd Floor			
; CITY: Chicago			
; STATE: Illinois			
; COUNTRY: USA			
; ZIP: 60606			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/537,361E			
; FILING DATE: 02-OCT-1995			
; CLASSIFICATION: 536			

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QY 1678 CAAACAAATTACCGCACTTCTGCTGAAGAGCAGAAAGCTGACCAACGAGCGGATGTC 1737
Db |||||
QY 1678 CAAAGCAATTACCGAATTTCTGCTGAAGAGCAGAAAGCTGACCAACGAGCGACTCC 1737
Db |||||
QY 1738 GGCTGTACTCAGATGAATTAATACTACTACGGTATGTGTAGCAATCTTTATCCGAAAAACCG 1797
Db |||||
QY 1738 GGCTGTACTCAGGAGAAATGCTACTACAGTATTTGTAGCGATCTTTAAGGAAAAAACTG 1797
Db |||||
QY 1798 GAATGGCAGATGCAAAATATCGATAAGCGCCGAATCCGTGCTTGTAGCTGACAGGCGGT 1857
Db |||||
QY 1798 GATTGGCAGATGAAAAATATGACAAAGCCAGAAATCCGCGGTATCGAGCTGACGGCGGT 1857
Db |||||
QY 1858 CTGAATGTGCAAAAGTAGGCTCTTTTGTCTCAGGCTGGAATTTGTCGGCTCGCTG 1917
Db |||||
QY 1858 CTGAATGTGCAAAAGTAGGCTCTTTTGTCTCAGGCTGGAATTTGTCGGCTCGCTG 1917
Db |||||
QY 1918 GGTATCGAAAAAGCAAACTGTGCGGCGCAACACAGCTGTGTCCACACAGCCCGCAAA 1977
Db |||||
QY 1918 GGTATCGAAAAAGCAAACTGTGCGGCGCAACACAGCTGTGTCCACACAGCCCGTGA 1977
Db |||||
QY 1978 GTGATTCGGGTGTGACTAGCAAGCCGAGCGCAAAATGGGGTGTGTTCTCCGCGCTG 2037
Db |||||
QY 1978 GTGATTCGGGTATCGACTATGAAGTCCGAGCGAAAAATGGGGCGTGTCTCTCCGCGCTG 2037
Db |||||
QY 2038 ACTTATCTGGGTGCAAAAAAGGCCAAAGACGCGCAATACACCGTTTATGAAAAACAAGSGC 2097
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QY 2158 GTGTTTGATATGATCGGCTTCTACAACTGGCTTAAAAAAGCTGCTGTCGAGCGGTA 2217
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QY 2338 CGTAAATACGCGGTATCGCTGGATGGAAGTTTGA 2373
Db |||||
QY 2338 CGTAAATACGCGGTATCGCTGGATGGAAGTTTGA 2373
Db |||||
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RESULT 9
US-08-817-707-3
; Sequence 3, Application US/08817707
; Patent No. 6277382
; GENERAL INFORMATION:
; APPLICANT: Stojiljkovic, Igor
; APPLICANT: So, Magdalene
; APPLICANT: Hwa, Vivian
; APPLICANT: Hefiron, Fred
; APPLICANT: Nassif, Xavier
; TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor
; TITLE OF INVENTION: Genes and Uses
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,707
; FILING DATE: 19-AUG-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6277382nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 94,784-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2373
; US-08-817-707-3
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Query Match 77.8%; Score 1849.6; DB 3; Length 2376;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 319; Indels 3; Gaps 1;

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Db |||||
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QY 181 ATTCAACAGAAATGATATACCGCAACAAAGAGCTTGTGCGTTACTCACGAGCTGCGC 240
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QY 481 AATTACCAAAACCCCTGCAAGGACATGATTTGCTGTGACGACAGCAATTCGGCGTGA 540
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QY 481 AATTACCAAAACCCCTGCAAGGACATGATTTGCTGTGACGACAGTTCGGCGTGA 540
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QY 541 ATGAAAAACCGTTTACAGCAGCGCAACCGGAATGGAACAATACACTCGGTTTCGGTGTG 600
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Db |||||
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STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,707
FILING DATE: 19-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6277382nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2373 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2370
US-08-817-707-5

Query Match      82.4%; Score 1958.4; DB 3; Length 2373;
Best Local Similarity 89.6%; Pred. No. 0;
Matches 2129; Conservative 0; Mismatches 241; Indels 6; Gaps 2;

QY 1 ATGAAACCAATTACATGCTTCTATFTGCCGCGCTGTCGGCAGTATTTTCGGCAATCCG 60
DB 1 ATGAAACCAATTACAAATGCTCCTATCTCGCGCGCTGTCGGCAGTATTTTCGGCAATCCG 60

QY 61 GTCTTGGCAGCGAGTGAAGCTGCAACCGCAACACACACCCGTTAAAGCAGAGATAAAGAA 120
DB 61 GTCTTGGCAGCGAGTGAAGCTGCAACTGAAACACACACCCGTTAAAGCAGAGATAAAGCA 120

QY 121 GTGCGGCTTAAAGACCCAGCTTAATGCGCTGCAACCGTGAACGCTGCAACCTCGCGCGC 180
DB 121 GTGCGGCTTAAAGCAGCGAGTGAAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 180

QY 181 ATTCAACAGGAATGATACGCGACCAACAAAGACTTGGTGGCTTACTCCACCGACGTCGCG 240
DB 181 ATCAACAGGAATGATACGCGACCAACAAAGACTTGGTGGCTTACTCCACCGATGTCGCG 240

QY 241 TTGAGGATAGCGCGCGCCATCAAAAGGCTTGTGTCGCGCGCGGTGGAAGCGCAACCGT 300
DB 241 TTGAGCGACAGCGCGCGCCATCAAAAGGCTTTCGCGCTTTCGCGCGGTGGAAGCGCAACCGT 300

QY 301 GTCGCTGTCAGATTTGACCGGCTGAGCGCTGCTGATTCGGAAGAAATCACTGCTATGCA 360
DB 301 GTCGCGTGAGCATAGACCGGCTTAAACCTGCTGATTCGGAAGAAATCACTGCTATGCGCC 360

QY 361 CGTTATGGCAACTTCAACAGCTCGCGCTGCTATGCAACCCGAACTCGTGGCGCAACATC 420
DB 361 CGTTATGGCAACTTCAACAGCTCGCGCTGCTATGCAACCCGAACTCGTGGCGCAACATC 420

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DB 421 GAAATCGTAAAGGCGCGACTCTTTCAATACCGGAGCGGCGCTTGGGCGCGCGTGTG 480

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DB 481 AATTACCAACCTTCAAGGACATGATTTGCTGTTGGATGATTCGGCGTGTG 540

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1561 ACTTACAAACCGGTTTCGGTAAATTCGCTGCTCCCAATCCCAACCTGAAAGCGGAGCGCAG 1620  
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1861 CGTCTGAATGTGACAAAAGTAGCGTCTTTTGTCTGAGGCTGGAATTTGTTCCGGCTCG 1920  
1915 CTGCGGTTATGCGAAAAAGCAAACTGTGCGGCGCAACAAGCCTGTCTCCACAGCGCGTG 1974  
1921 CTGCGGTTATGCGAAAAAGCAAACTGTGCGGCGCAACAAGCCTGTCTCCACAGCGCGTG 1980  
1975 AAAGTGAATGCGCGGTGCTGACTAGCAAGCGCGGAGGAAATGCGGTGCTTCTCCCGC 2034  
1981 AAAGTGAATGCGCGGTATCGACTATGAAAGTCCGAGCGGAAATGCGGCGGTGTTCTCCCGC 2040  
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2335 GCGCGTAAATTAACCGCTTATCGCTGGAATGGAAGTTTGA 2373  
2341 AGCGTAAATTAACCGCTTATCGCTGGAATGGAAGTTTGA 2379

## RESULT 8

US-08-817-707-5  
; Sequence 5, Application US/08817707  
; Patent No. 6277382  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor  
; TITLE OF INVENTION: Genes and Uses  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boenken Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago

QY 1495 CATGCGGTACGACATTAATTCCTCGGTACCGTCCCAATGCGTCCGAAGTATTTTC 1554  
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QY 1555 ACTTAAACACCGGTTCGGTAAATTCCTCGGTACCGTCCCAATGCGTCCGAAGTATTTTC 1614  
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QY 1675 TATCAAAACAAATACCGCAATTCCTGCTGAAGAGCAGCAAGTCAACACCGCGCGAT 1734  
DB 2151 TATCAAAACAAATACCGCAATTCCTGCTGAAGAGCAGCAAGTCAACACCGCGCGAT 2210  
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QY 2335 GCGCGTAATTCGCGTATCGCTGATTCGAGTTTGA 2373  
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## RESULT 7

US-08-537-361E-5

; Sequence 5, Application US/08537361E

; Patent No. 6121037

; GENERAL INFORMATION:

; APPLICANT: Stojiljkovic, Igor

; APPLICANT: So, Magdalene

; APPLICANT: Hwa, Vivian

; APPLICANT: Heffron, Fred

; APPLICANT: Nassif, Xavier

; TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor

; TITLE OF INVENTION: Genes and Uses  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/537,361E  
; FILING DATE: 02-OCT-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6121037nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 94,784-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2379 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2376  
; US-08-537-361E-5

Query Match 83.4%; Score 1983.8; DB 3; Length 2379;

Best Local Similarity 90.2%; Pred. No. 0;

Matches 2146; Conservative 0; Mismatches 227; Indels 6; Gaps 2;

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DB 1 ATGAACCATTAACATCTTCTTATTCGCGCTGTCGCGAGTATTTTCGGCAATCCG 60

QY 61 GTCTTGGCAGCGGATGAAGCTGCAACCCGCAACCCGCTTAAAGCAGAGATAAAGAA 120

DB 61 GTCTTGGCAGCGGATGAAGCTGCAACCCGCAACCCGCTTAAAGCAGAGATAAAGAA 120

QY 121 GTGCGCGTTAAAGACCAAGCTTAATCGCGCTGCAACCCGCTGGAACGCTCAACCTCGGCGC 180

DB 121 GTGCGCGTTAAAGACCAAGCTTAATCGCGCTGCAACCCGCTGGAACGCTCAACCTCGGCGC 180

QY 181 ATTCAACAGGAAATGATACGGGCAACAAAGACTTTGGTGGTACTTCCACCGACGTCGCG 240

DB 181 ATCAAAACAGGAAATGATACGGGCAACAAAGACTTTGGTGGTACTTCCACCGACGTCGCG 240

QY 241 TTGAGCGATAGCGCGCGCCATCAAAAGGCTTTGCTGCGCGGCTGGAAGGCAACCGT 300

DB 241 TTGAGCGATAGCGCGCGCCATCAAAAGGCTTTGCTGCGCGGCTGGAAGGCAACCGT 300

QY 301 GTCGCGTGTGAGCATTTGACGGCGTGAAGCTGCTGATTTGGAGAGAAATCTCACTGTATGCA 360

DB 301 GTCGCGTGTGAGCATTTGACGGCGTGAAGCTGCTGATTTGGAGAGAAATCTCACTGTATGCA 360

QY 361 GCTTATGGCAATTCACAGCTCGCGCTGCTATTCGACCCCGCAACTGTCGGCGCAATC 420

DB 361 GCTTATGGCAATTCACAGCTCGCGCTGCTATTCGACCCCGCAACTGTCGGCGCAATC 420

QY 421 GAAATCGCGAGGCGCTGACTCTTTCAATACCGGTAGCGGCGCATTTGGTGGCGCGTG 480

DB 421 GACATCGTAAAGGGGCGGACTCTTTCAATACCGGTAGCGGCGCATTTGGTGGCGCGTG 480

APPLICANT: Stojiljkovic, Igor  
 APPLICANT: So, Magdalena  
 APPLICANT: Hwa, Vivian  
 APPLICANT: Heffron, Fred  
 APPLICANT: Nassif, Xavier  
 TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor  
 TITLE OF INVENTION: Genes and Uses  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
 STREET: 300 South Wacker Drive, 32nd Floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/537,361E  
 FILING DATE: 02-OCT-1995  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 6121037nan, Kevin E  
 REGISTRATION NUMBER: 35,303  
 REFERENCE/DOCKET NUMBER: 94,784-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-913-0001  
 TELEFAX: 312-913-0002  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3319 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 471..2848  
 US-08-537-361E-1

Query Match 83.5%; Score 1985.4; DB 3; Length 3319;  
 Best Local Similarity 90.2%; Pred. No. 0;  
 Matches 2147; Conservative 0; Mismatches 226; Indels 6; Gaps 2;

Qy 1 ATGAAACCATTTACATGCTTCTTATTTGCGCGCTGCTGGCGAGTATTTTCGGCAATCCG 60  
 Db 471 ATGAAACCATTTACAAATGCTCCCTATCGCGCGCTGCTGGCGAGTATTTTCGGCAATCCG 530  
 Qy 61 GTCTTGGCAGGATGAGCTGCACCAACCAACACACCCGTTAAAGCAGATATAAGAA 120  
 Db 531 GTCTTGGCAGATGAGCTGCACCAACCAACCAACACCCGTTAAAGCAGATATAAGAA 590  
 Qy 121 GTGCGCGTTAAAGACCAACAGCTTAATGCGCGCTGCACACCGTGTGCAACCTCGGCGCG 180  
 Db 591 GTGCGCGTTAAAGACCAACAGCTTAATGCGCGCTGCACACCGTGTGCAACCTCGGCGCG 650  
 Qy 181 ATTCAACAGGAATGATACCGGCAACAAAGACTTGTGTGGTGTACTCCACCGAGCTCGGC 240  
 Db 651 ATCAAAACAAGAAATGATACCGGCAACAAAGACTTGTGTGGTGTACTCCACCGAGCTCGGC 710  
 Qy 241 TTGAGCGATAGCGCGCCCATCAAAAGGCTTTGCTGTGCGCGCGTGGAGGCAACCGT 300  
 Db 711 TTGAGCGATAGCGCGCCCATCAAAAGGCTTTGCTGTGCGCGCGTGGAGGCAACCGT 770  
 Qy 301 GTGCGTGTGAGCATGACGCGCTGAGCGCTGCTGATTCGGAAGAAACTCACTGTATGCA 360  
 Db 771 GTGCGTGTGAGCATGACGCGCTGAGCGCTGCTGATTCGGAAGAAACTCACTGTATGCA 830  
 Qy 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATGACCCCGCAACTCTGTCGGCAATC 420

Db 831 CGTTATGGCAACTTCAACAGCTCGCGTCTGTCTATGACCCCGCAACTCTGTCGCAACATC 890  
 Qy 421 GAAATGCGGAAGCGCGCTGACTCTTTCAATACCGTAGCGCGCATGTTGGTGGCGGCTG 480  
 Db 891 GACATGTTAAAGGGCGGACTCTTTCAATACCGTAGCGCGCATGTTGGTGGCGGCTG 950  
 Qy 481 AATTACCAACCCCTGCAAGGACATGTTTCTGTTGAGCAGCAGGCAATTCGCGCTGATG 540  
 Db 951 AATTACCAACCCCTGCAAGGACATGTTTCTGTTGAGCAGCAGGCAATTCGCGCTGATG 1010  
 Qy 541 ATGAAACCGTTACAGACCGCGCAACCGGAGTGAACAAATACACTCTCGTTCGTTGCTG 600  
 Db 1011 ATGAAACCGTTACAGACCGCGTAAACCGTGAATGGAACAATACCTTCGCTTCGCGCTG 1070  
 Qy 601 AGCAACGACCGCTGGATGCGCTTCTGCTATTTCGCAACGTCGCGTCAATGACAGCAAA 660  
 Db 1071 AGCAACGACCGCTGGATGCGCTTCTGCTATTTCGCAACGTCGCGTCAATGACAGCAAA 1130  
 Qy 661 AGCGCGGCGAGCGTGCCTATCCGCTAGAGGGTCTGGCAGCGGAGCAATTCCTCGTGGT 720  
 Db 1131 AGCGCGGCGAGCGTGCCTATCCGCTAGAGGGTCTGGTAGCGGAGCAATTCCTCGTGGT 1190  
 Qy 721 TCGTACGCGGTATCCCTGATCCGTCGAACACAAATACACAACTCTTTCGGTAAAGATT 780  
 Db 1191 TCTGCGCGGCTATTCCTGATCCGTCGCAACACAAATACACAACTCTTTCGGTAAAGATT 1250  
 Qy 781 GCTTATCAAAATCAACGACAGCAGCAGCATCGGCCATCGTTTAAACGCGCAGAGGGGCAT 840  
 Db 1251 GCTTATCAAAATCAACGACAGCAGCAGCATCGGCCATCGCTCAACGCTAGAGGGGCAT 1310  
 Qy 841 AATTACACGATTGAAGAGTCTTATAACCTGACCGCTTCTTCTGCGCGAGCGAGTGAC 900  
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 Db 1371 GTCAACAGACGCGGTAACACCAACCTCTTTTACGAAATGGAACGCGGAATCCGACCGGTTG 1430  
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 Qy 1021 GGCTCGTTCCCGA --- CGGATTATTCACCTGGACCGCGCAACTATATATCAGAGAGATTG 1077  
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 Db 1671 CGCGCTGATTTTGAACCTTAAACCGCGAGATTATTTACTTTCAGCGCGCTGTGTGTTGGA 1730  
 Qy 1255 ACTACAGCTGATTCAACACCCGCTGAAAACCACTAAATATTTGTTCTCACTGTCTGAT 1314  
 Db 1731 ACCACGAGCAGTATCCAGCATCCGCTGAAAACCAACCACTACCGTTTCTCACTGTCTGAC 1790  
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301 GTGGGTGTCAGCAATGACGGCTGAGCTGCTGCTGATTCGGAAGAAATCACTGATGCA 360  
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770 GTGGGTGTCAGCAATGACGGCTGAGCTGCTGATTCGGAAGAAATCACTGATGCA 829  
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361 CGTTATGGCAATTCAGAGCTGGCGCTGCTATGAGACCCGGAATCTGGTGGCAATATC 420  
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830 CGTTATGGCAATTCAGAGCTGGCGCTGCTATGAGACCCGGAATCTGGTGGCAATATC 889  
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481 AATTACCAACCTGCAAGGACATGATTTGCTTTGGACAGCAGGCAATTCGGCGTATG 540  
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541 ATGAAACCGGTACAGAGCGGCAACCGGCAATGGAACAAATACACTCGGTTTCGGTGTG 600  
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601 AGCAACGACCGGTGATGCGCTTTGCTGATTCGCAACGTCGCGGTCAATCAGACCGAA 660  
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1070 AGCAACGACCGGTGATGCGCTTTGCTGATTCGCAACGTCGCGGTCAATCAGACCGAA 1129  
QY  
661 AGCGCGGCGAGCTGGCTATCCGGTAGAGGTGCTGGCAGCGGAGCAATTAATCCGTGT 720  
Db  
1130 AGCGCGGCGAGCTGGCTATCCGGTAGAGGTGCTGGCAGCGGAGCAATTAATCCGTGT 1189  
QY  
721 TCGTACGCGGTATCCGTATCCGGTAGAGGTGCTGGCAGCGGAGCAATTAATCCGTGT 780  
Db  
1190 TCGTACGCGGTATCCGTATCCGGTAGAGGTGCTGGCAGCGGAGCAATTAATCCGTGT 1249  
QY  
781 GCTTATCAATCAACGACGACCGCATCGGCCATCGTTTAAACGGCGCAGCGGCGAT 840  
Db  
1250 GCTTATCAATCAACGACGACCGCATCGGCCATCGTTTAAACGGCGCAGCGGCGAT 1309  
QY  
841 AATTACGAGTGAAGAGTCTTAACTGACCGCTTTCTTCTGGCGGAGACCGCATGAC 900  
Db  
1310 AATTACGAGTGAAGAGTCTTAACTGACCGCTTTCTTCTGGCGGAGACCGCATGAC 1369  
QY  
901 GTAACAGAGCGGCAATGCGCAACCTTTTACGATGAGACCGCTGATTCAAATTTGGCTG 960  
Db  
1370 GTAACAGAGCGGCAATGCGCAACCTTTTACGATGAGACCGCTGATTCAAATTTGGCTG 1429  
QY  
961 TCGTCTTTGAGCGGCAATGCGCAACCTTTTACGATGAGACCGCTGATTCAAATTTGGCTG 1020  
Db  
1430 TCGTCTTTGAGCGGCAATGCGCAACCTTTTACGATGAGACCGCTGATTCAAATTTGGCTG 1489  
QY  
1021 GGCTCGTTCGCA --- CGGATTAATCCAGTGGACGCGCACTATTAATCAGAGGATTTG 1077  
Db  
1490 GGCTCGTTCGCA --- CGGATTAATCCAGTGGACGCGCACTATTAATCAGAGGATTTG 1549  
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1078 GAGATATATACACCGGAGATGAGACCGGCAATTCGATTTTACCTTTGGTGGATGAC 1137  
Db  
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Db  
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1255 ACTACAGCTCGATTCAGACCGGCGGAGACCGGCAATTAATTAATTCAGCGGAGAGATTCGCGT 1314  
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1315 CAAATCCATGAAACGAGCTGTTTACGACCGGCGGAGATTCGCTTACGATCATACCAAA 1374  
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1790 CAAATCCATGAAACGAGCTGTTTACGACCGGCGGAGATTCGCTTACGATCATACCAAA 1849  
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1615 ACCACCCACCGCTGCTCTGCAAGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1674  
Db  
2090 ACCACCCACCGCTGCTCTGCAAGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2149  
QY  
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Db  
2150 TATCAAAACAAATTAACCGCAACTTTCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 2209  
QY  
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Db  
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1795 CCGGATGCGAGATGCAAAATATCGATAAGGCGGCAATTCGCTGAGGCTGGAATTTGCTGGCTG 1854  
Db  
2270 CCGGATGCGAGATGCAAAATATCGATAAGGCGGCAATTCGCTGAGGCTGGAATTTGCTGGCTG 2329  
QY  
1855 CGTCTGAATGTGACAAAAGTAGCGCTTTTCTGCTGAGGCTGGAATTTGCTGGCTG 1914  
Db  
2330 CGTCTGAATGTGACAAAAGTAGCGCTTTTCTGCTGAGGCTGGAATTTGCTGGCTG 2389  
QY  
1915 CTGGTTATGCGAAAAGCAAACTGTGCGGCGACAAACGCTGCTCTCCACACAGCGCGG 1974  
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2390 CTGGTTATGCGAAAAGCAAACTGTGCGGCGACAAACGCTGCTCTCCACACAGCGCGG 2449  
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1975 AAGTGATTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2034  
Db  
2450 AAGTGATTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2509  
QY  
2035 CTGACTTATCTGGGTGCGAAAAGGCGCAAGACGCGCAATACACCGCTTTATGAAACCAAG 2094  
Db  
2510 CTGACTTATCTGGGTGCGAAAAGGCGCAAGACGCGCAATACACCGCTTTATGAAACCAAG 2569  
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Db  
2570 GCGTGGGGTACGCTTTTGCAGAAAAGGTAAGATTAACCGTGGCTGCAACGATCGGCT 2629  
QY  
2155 TATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2214  
Db  
2630 TATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2689  
QY  
2215 GTATATAATGTGTTTCAACCGCAAAATACACCTTTGGGATTTCCCTCGCGGGTTTGTATAGC 2274  
Db  
2690 GTATATAATGTGTTTCAACCGCAAAATACACCTTTGGGATTTCCCTCGCGGGTTTGTATAGC 2749  
QY  
2275 TACAGCACCAACCGCGGCTGACCGGATGGAAGGCTTTAGACCGCTTACCGCGCTCA 2334  
Db  
2750 TACAGCACCAACCGCGGCTGACCGGATGGAAGGCTTTAGACCGCTTACCGCGCTCA 2809  
QY  
2335 GCGCGTAAATACCGGCTATCGCTGATTTGGAAGTTTTCGA 2373  
Db  
2810 AGCGGTAATACCGGCTATCGCTGATTTGGAAGTTTTCGA 2848

## RESULT 6

US-08-537-361E-1

; Sequence 1, Application US/08537361E

; Patent No. 6121037

; GENERAL INFORMATION:





QY	2335	GGCCGTAATTACGCCGTAATCGCTGATTTGGAAGTTTGA	2373
Db	2810	AGCCGTAATTACGCCGTAATCGCTGGAATGGAATTTAA	2848
RESULT 4			
US-08-817-707-1			
; Sequence 1, Application US/08817707			
; Patent No. 6277382			
; GENERAL INFORMATION:			
; APPLICANT: Stojiljkovic, Igor			
; APPLICANT: So, Magdalena			
; APPLICANT: Hwa, Vivian			
; APPLICANT: Heffron, Fred			
; APPLICANT: Nassif, Xavier			
; TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor			
; TITLE OF INVENTION: Genes and Uses			
; NUMBER OF SEQUENCES: 15			
; CORRESPONDENCE ADDRESSES:			
; ADDRESS: 300 South Wacker Drive, 32nd Floor			
; CITY: Chicago			
; STATE: Illinois			
; COUNTRY: USA			
; ZIP: 60606			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/817,707			
; FILING DATE: 19-AUG-1997			
; CLASSIFICATION: 424			
; ATTORNEY/AGENT INFORMATION:			
; NAME: No. 6277382nan, Kevin E			
; REGISTRATION NUMBER: 35,303			
; REFERENCE/DOCKET NUMBER: 94,784-J			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 312-913-0001			
; TELEFAX: 312-913-0002			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 3318 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
; HYPOTHETICAL: NO			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 470..2845			
US-08-817-707-1			
Query Match 83.7%; Score 1990.2; DB 3; Length 3318;			
Best Local Similarity 90.4%; Pred.No. 0;			
Matches 2150; Conservative 0; Mismatches 223; Indels 6; Gaps 2;			
QY	1	ATGAAACCAATTACATGCTTCTCTATTCCCGCGCTGGTGGCAGTATTTTCGGCAATCCG	60
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Db	530	GTCTTGGCGCAGATGAAGCTGCAACTGAAACCAACCAACCGGTTAAAGCAGAGGTAAGCA	589
QY	121	GTGCGGTTAAAGACCACTTAATCGCGCTGCAACCGTGGAACGTGTCAACCTCGCGCG	180
Db	590	GTGCGGTTAAAGGCGAGCGCAATCGCGCTGTGGAAACGCGTCAACCTTTAACCGT	649
QY	181	ATTCAACAGGAAATGATACGCGCAACAAAGACTTGGTGGTACTCCACCGACGTCGCG	240

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Db 650 ATCAAAACAGAAATGATACCGGACCAAGAGCTTGGTGGTACTCCACCGATGTGGC 709  
Qy 241 TTGAGCGATACGCGCGCCCAATCAAAAGGCTTTGCTGTGCGCGCGTGGGAAGGCAACCGT 300  
Db 710 TTGAGCGACAGCGCGCCCAATCAAAAGGCTTTGCTGTGCGCGCGTGGGAAGGCAACCGT 769  
Qy 301 GTCGGTGTGACATGTGACGCGGTGAGCTCTCTGATTCGGAAGAAACTCACTGTATGCA 360  
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Qy 361 GGTATGCGAACTTCAACAGCTGCGGCTGTCTATCGACCCCGAACTCGTGGCGCAATC 420  
Db 830 GGTATGCGAACTTCAACAGCTGCGGCTGTCTATCGACCCCGAACTCGTGGCGCAATC 889  
Qy 421 GAAATCGGAAGGCGCTGACTCTTCAATACGCTGAGCGCGCATTTGGGTGGCGCGTG 480  
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Qy 481 AATTACCAAACTTCAAGGACATGATTTGCTGTGAGGACGAGCAATTCGCGGTGATG 540  
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Qy 541 ATGAAAACGGTTACAGCAGCGCAACCGCGAATGGAATAATACATCTCGGTTTCGGTGTG 600  
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Db 1970 CGTGTCCGTTTACGACATTTACTTCCGCTACCGTGTCCCAATCGTCCGAAGTGTATTC 2029  
Qy 1555 ACTTACAAACACGCTTGGGTAAATGGCTCCCAATCCCACTGAAAGCGGAGCGCAGC 1614  
Db 2030 ACTTACAAACACGCTTGGGTAAATGGCTCCCAATCCCACTGAAAGCGGAGCGCAGC 2089  
Qy 1615 ACCACCCACACCTGTCTCTGCAAGCGCGCAGGAGGAGTACTTTGGATGCGCAACTG 1674  
Db 2090 ACCACCCACACCTGTCTCTGCAAGCGCGCAGGAGGAGTACTTTGGATGCGCAACTG 2149  
Qy 1675 TATCAAAACAAATTACCGCAACTTCTTGTCTGAAGAGCAGAGCTGACCAACGCGCGAT 1734  
Db 2150 TATCAAAACAAATTACCGCAACTTCTTGTCTGAAGAGCAGAGCTGACCAACGCGCGAT 2209  
Qy 1735 GTCGCTGTACTCAGATGAATTACTACTAGCGTATGTGTAGCAATCTTATTCGAAAAA 1794  
Db 2210 GTCAGCTGTACTCAGATGAATTACTACTAGCGTATGTGTAGCAATCTTATTCGAAAAA 2269  
Qy 1795 CCGGAATGGCAGATGCAAAATATCGATAAGCGCCGAATCCGTGTCTGTAGCTGACAGGC 1854  
Db 2270 CTGGAATGGCAGATGCAAAATATCGACAGCGCAGAAATCCGCGTCTGAGCTGACGGC 2329  
Qy 1855 CGTCTGAATGTGACAAAGTGTCTTTTCTTCTGAGGCTTGAATAATTTTCTGGGTCTG 1914  
Db 2330 CGTCTGAATGTGACAAAGTGTCTTTTCTTCTGAGGCTTGAATAATTTTCTGGGTCTG 2389  
Qy 1915 CTGCGTTATCGAAAAAGCAAACTGTGCGGCGCAACACGCTGTCTGTCCACAGCCCGC 1974  
Db 2390 CTGCGTTATCGAAAAAGCAAACTGTGCGGCGCAACACGCTGTCTGTCCACCGCGCTG 2449  
Qy 1975 AAAGTGAATTCGCGGTGTGCACTACGAAAGCGCGAGGAAAAATGGGGTGTGTCTCCCGC 2034  
Db 2450 AAAGTGAATTCGCGGTGTGCACTATGAAAGTCCGAGCGAAAAATGGGGCGTGTCTCCCGC 2509  
Qy 2035 CTGACTTATCTGCGGTGCGAAAAAGGCGCAATACACCGTGTATGAAAAACAAG 2094  
Db 2510 CTGACTTATCTGCGGTGCGAAAAAGGTCAAAGACGCGCAATACACCGTGTATGAAAAACAAG 2569  
Qy 2095 GCGCGGCTACGCGTTTTCGAAAAAGGTTAAAGATTAACCGTGTGTGAACAAGTCCGCT 2154  
Db 2570 GCGTGGGTACGCGTTTTCGAAAAAGGTTAAAGATTAACCGTGTGTGAACAAGTCCGCT 2629  
Qy 2155 TATGTGTTTGAATGTACGCGTCTTCAAACTGCTAAAAACCTGACTTTTTCGCTGACGCC 2214  
Db 2630 TATGTGTTTGAATGTACGCGTCTTCAAACTGCTAAAAACCTGACTTTTTCGCTGACGCC 2689  
Qy 2215 GTATATAATGTGTTCAAACCGCAATACCACTTTGGGATTTCCCTGCGCGGTGTGTATAGC 2274  
Db 2690 GTATATAATGTGTTCAAACCGCAATACCACTTTGGGATTTCCCTGCGCGGTGTGTATAGC 2749  
Qy 2275 TACAGACCAACCAACCGGTGACCGGATGGAAGGCTTAGACCGCTACCGCGCTCA 2334  
Db 2750 TACAGACCAACCAACCGGTGACCGGATGGAAGGCTTAGACCGCTACCGCGCTCA 2809

Db 1141 CAAACCGTTGCAACTGGGCGCCCAACATCGCTTGTGCTTAAAACTTTGCCAGTCCGGT 1200  
QY 1201 GAGTTTGAACCTTAAACCGCGACGATTAATCTTACGCGAAGAGTATCCCGTACTACC 1260  
Db 1201 GAGTTTGAACCTTAAACCGCGACGATTAATCTTACGCGAAGAGTATCCCGTACTACC 1260  
QY 1261 AGCTGATTCACACACCCCGTGAACCACTAATATATGTTTCTCACTGCTCATCAAAATC 1320  
Db 1261 AGCTGATTCACACACCCCGTGAACCACTAATATATGTTTCTCACTGCTCATCAATC 1320  
QY 1321 CAATGAACGAGTGTTCAGACGCGTGCAGATATCCGTTACGATCATACCAAAATGAGC 1380  
Db 1321 CAATGAACGAGTGTTCAGACGCGTGCAGATATCCGTTACGATCATACCAAAATGAGC 1380  
QY 1381 CCTCAGGAATTCAGTCCGAGTGTATGCTTGTGCAAAACACCGCTGCAGCCCAATCT 1440  
Db 1381 CCTCAGGAATTCAGTCCGAGTGTATGCTTGTGCAAAACACCGCTGCAGCCCAATCT 1440  
QY 1441 TATAAGGCTGAGCGGATTTGCTGCTTTGGCGGCGCAACTGAATCAGGCTTGGCATGTC 1500  
Db 1441 TATAAGGCTGAGCGGATTTGCTGCTTTGGCGGCGCAACTGAATCAGGCTTGGCATGTC 1500  
QY 1501 GGTACGACATTAATTCGCGCTACGCTGCTCCCAATGCTCCGAAGTGTATTTCACTTAC 1560  
Db 1501 GGTACGACATTAATTCGCGCTACGCTGCTCCCAATGCTCCGAAGTGTATTTCACTTAC 1560  
QY 1561 AACCCGCTGCGGTAAATGCTGCTCCCAATCCCACTGAAAGCGGCGAGCACCAACC 1620  
Db 1561 AACCCGCTGCGGTAAATGCTGCTCCCAATCCCACTGAAAGCGGCGAGCACCAACC 1620  
QY 1621 CACACCTGCTCTGCAAGCGCGAGCGAAAGGTACTTTGATGCCAACCTGTATCAA 1680  
Db 1621 CACACCTGCTCTGCAAGCGCGAGCGAAAGGTACTTTGATGCCAACCTGTATCAA 1680  
QY 1681 AACCAATTCGCAACTTTTGTCTGAAGAGCAAGAGTGCACCAAGCGGCGATGTCGCG 1740  
Db 1681 AGCAATTCGCAAACTTTTGTCTGAAGAGCAAGAGTGCACCAAGCGGCGATGTCGCG 1740  
QY 1741 TGCTACTCAGTCAATTAATCTACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
Db 1741 TGCTACTCAGTCAATTAATCTACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
QY 1801 TGGCAGATGCAAAATATCGATAAGGCCCGCAATCCGTTGCTGCTGCTGCTGCTGCTG 1860  
Db 1801 TGGCAGATGCAAAATATCGATAAGGCCCGCAATCCGTTGCTGCTGCTGCTGCTGCTG 1860  
QY 1861 AATGTGACAAAGTAGCGTCTTTGTTCTGAGGCTGGAATTTGTTGCTGCTGCTGCTG 1920  
Db 1861 AATGTGACAAAGTAGCGTCTTTGTTCTGAGGCTGGAATTTGTTGCTGCTGCTGCTG 1920  
QY 1921 TATGCGAAAGCAAACTGTGCGGCGACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980  
Db 1921 TATGCGAAAGCAAACTGTGCGGCGACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980  
QY 1981 ATTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
Db 1981 ATTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
QY 2041 TATCTGGGTGCAAAAGGCGCAACGCGCAATACACCGTTTATGAAACAAAGGCGCGG 2100  
Db 2041 TATCTGGGTGCAAAAGGCGCAACGCGCAATACACCGTTTATGAAACAAAGGCGCGG 2100  
QY 2101 GGTACGCTTTTCGAAAGAGTAAAGNTTACCGTGGCTGCAACAGTCCGCTTATGTCG 2160  
Db 2101 GGTACGCTTTTCGAAAGAGTAAAGNTTACCGTGGCTGCAACAGTCCGCTTATGTCG 2160  
QY 2161 TTTGATATGTCGCTTTTACAAATCGGCTAATAACCTGCTGCTGCTGCTGCTGCTGCTG 2220  
Db 2161 TTTGATATGTCGCTTTTACAAATCGGCTAATAACCTGCTGCTGCTGCTGCTGCTGCTG 2220  
QY 2221 AATGTGTTCAACCGCAAAATACCACTTGGGATTCCTGCGCGGTTTGTATAGCTACAGC 2280

Db 2221 AATGTGTTCAACCGCAAAATACCACTTGGGATTCCTGCGCGGTTTGTATAGTACACC 2280  
QY 2281 ACCACCAACGCGTGCAGCGAGATGCAAGGCTTTAGACCGCTACCGGCGCTCAGGCGCT 2340  
Db 2281 ACCACCAACGCGTGCAGCGAGATGCAAGGCTTTAGACCGCTACCGGCGCTCAGGCGCT 2340  
QY 2341 AATTACGCGGTATCGCTGCTGATTTGGAAGTTTGAATTC 2378  
Db 2341 AATTACGCGGTATCGCTGCTGATTTGGAAGTTTGAATTC 2378

RESULT 3  
US-08-990-470A-1  
; Sequence 1, Application US/08990470A  
; Patent No. 6123942  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6123942el Bacterial Hemoglobin Receptor  
; TITLE OF INVENTION: Genes and Uses  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/990,470A  
; FILING DATE: 15-DEC-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6123942nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 94,784-K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3318 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 470..2845  
; US-08-990-470A-1

Query Match 83.7%; Score 1990.2; DB 3; Length 3318;  
Best Local Similarity 90.4%; Pred. No. 0;  
Matches 2150; Conservative 0; Mismatches 223; Indels 6; Gaps 2;  
QY 1 ATGAACCATTTACATGCTTCTTATTCGCGGCTGCTGCGGAGTATTTTCGGCAATCCG 60  
Db 470 ATGAACCATTTACAAATGCTCCCTATTCGCGGCTGCTGCGGAGTATTTTCGGCAATCCG 529  
QY 61 GTCTTGGCAGCGGATGAAGCTGCAACCGCAACCGGCTTTAAAGCAGAGATAAAGAA 120  
Db 530 GTCTTGGCAGAGTGAAGCTGCAACTGAACACCGGCTTTAAAGCAGAGATAAAGCA 589  
QY 121 GTGCGCGTTAAAGACCACTTAATGCGGCTTAATGCGGCTGCAACCGTGAACGCTGTCAACCTCGGCGC 180

QY 2161 TTGTATATGACGGCTTCTACAACTGGCTAAACCTGACTTTGCGTGCAGGCGTATAT 2220  
Db 2161 TTGTATATGACGGCTTCTACAACTGGCTAAACCTGACTTTGCGTGCAGGCGTATAT 2220  
QY 2221 AATGTGTTCAACCGCAATACACACCTTGGGATTCCTCGCGGTTTGTATAGCTACAGC 2280  
Db 2221 AATGTGTTCAACCGCAATACACACCTTGGGATTCCTCGCGGTTTGTATAGCTACAGC 2280  
QY 2281 ACCACCAACCGGTGCGACCGAGATGCGAAAGGCTTAGACCGCTACCGCGCTCAGGCCGT 2340  
Db 2281 ACCACCAACCGGTGCGACCGAGATGCGAAAGGCTTAGACCGCTCAGGCCGT 2340  
QY 2341 AATTACCGCTATCGCTGGATTTGAAGTTTGAATTC 2378  
Db 2341 AATTACCGCTATCGCTGGATTTGAAGTTTGAATTC 2378

## RESULT 2

US-08-537-361E-7  
; Sequence 7, Application US/08537361E  
; Patent No. 6121037  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor  
; TITLE OF INVENTION: Genes and Uses  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/537,361E  
; FILING DATE: 02-OCT-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6121037nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 94,784-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2378 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2370  
US-08-537-361E-7

Query Match 99.2%; Score 2358.8; DB 3; Length 2378;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2366; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
QY 1 ATGAACCAATACACATGCTTCTTATTCGCGCTGTCGCGAGTATTTTCGGCAATCCG 60  
Db 1 ATGAACCAATACACATGCTTCTTATTCGCGCTGTCGCGAGTATTTTCGGCAATCCG 60

QY 61 GTCTTGGCAGCGGATGAAGCTGCAACCGAAACCAACCCCTTTAAAGCAGAGATAAAAGAA 120  
Db 61 GTCTTGGCAGCGGATGAAGCTGCAACCGAAACCAACCCCTTTAAAGCAGAGATAAAAGAA 120  
QY 121 GTGCGGTTTAAAGACGAGCTTAATGCGCTGCAACCGTGGAACTGTCACTCGGCGCG 180  
Db 121 GTGCGGTTTAAAGACGAGCTTAATGCGCTGCAACCGTGGAACTGTCACTCGGCGCG 180  
QY 181 ATTCAACAGCAAAATGATACGCGACAAACAAAGACTTGGTGTGTTACTCCACCGAGCTCGGC 240  
Db 181 ATTCAACAGCAAAATGATACGCGACAAACAAAGACTTGGTGTGTTACTCCACCGAGCTCGGC 240  
QY 241 TTGAGCGATAGCGCGCCCATCAAAAGGCTTTGCTGTGCGCGCGTGGAAAGCAACCGT 300  
Db 241 TTGAGCGATAGCGCGCCCATCAAAAGGCTTTGCTGTGCGCGCGTGGAAAGCAACCGT 300  
QY 301 GTCGGTGTACGATTTGACGCGGTGAGCTGCTGATTCGGAAGAAACTCACTGTATGCA 360  
Db 301 GTCGGTGTACGATTTGACGCGGTGAGCTGCTGATTCGGAAGAAACTCACTGTATGCA 360  
QY 361 CGTTATGGCAACTTCAACAGCTCGCGCTCTCTATCGACCCCGAACTCGTGGCGCAATC 420  
Db 361 CGTTATGGCAACTTCAACAGCTCGCGCTCTCTATCGACCCCGAACTCGTGGCGCAATC 420  
QY 421 GAAATCGCGAAGGCGCTGACTCTTTCAATACCGGTAGCGCGCATTTGGGTGGCGGCTG 480  
Db 421 GAAATCGCGAAGGCGCTGACTCTTTCAATACCGGTAGCGCGCATTTGGGTGGCGGCTG 480  
QY 481 AATTACCAACCTTCAACAGCATGATTTGCTGTGAGACGACAGGCAATTCGCGGTGATG 540  
Db 481 AATTACCAACCTTCAACAGCATGATTTGCTGTGAGACGACAGGCAATTCGCGGTGATG 540  
QY 541 ATGAAAAACGTTTACAGCAGCGCAACCGCAATGCAAAATACACTCGGTTCGCGTGTG 600  
Db 541 ATGAAAAACGTTTACAGCAGCGCAACCGCAATGCAAAATACACTCGGTTCGCGTGTG 600  
QY 601 AGCAACGACCGGTGATGCGCTTTGCTGTATTCGCAACGTCGCGGTCAATGACGCA 660  
Db 601 AGCAACGACCGGTGATGCGCTTTGCTGTATTCGCAACGTCGCGGTCAATGACGCA 660  
QY 661 AGCGCGGCGAGCGTGGCTATCCGTAGAGGCTGCTGGAGCGGAGCAATATCCGTTG 720  
Db 661 AGCGCGGCGAGCGTGGCTATCCGTAGAGGCTGCTGGAGCGGAGCAATATCCGTTG 720  
QY 721 TCCTACGCGGTATCCCTGATCCGTCACAAACACAAATACCAAACTCTCTTGGGTAAAGAT 780  
Db 721 TCCTACGCGGTATCCCTGATCCGTCACAAACACAAATACCAAACTCTCTTGGGTAAAGAT 780  
QY 781 GCTTATCAATCAACGACAGCAGCAGCGCATCGGCCCATCGTTTAAACGCGCAGCGGCGCAT 840  
Db 781 GCTTATCAATCAACGACAGCAGCAGCGCATCGGCCCATCGTTTAAACGCGCAGCGGCGCAT 840  
QY 841 AATTACAGATTGAAGCTTTATACCTGACCGCTTCTTCTGGCGCGAGCGCATGAC 900  
Db 841 AATTACAGATTGAAGCTTTATACCTGACCGCTTCTTCTGGCGCGAGCGCATGAC 900  
QY 901 GTAAACAGACGCGCAATGCAACCTTTTACGAATGAGCGCTGATTCAAATGCGCTG 960  
Db 901 GTAAACAGACGCGCAATGCAACCTTTTACGAATGAGCGCTGATTCAAATGCGCTG 960  
QY 961 TCCTCTTTGAAAGCGGATTCGATTTATCAGCAACCAAAAGTGGCGGCTTAAACAA 1020  
Db 961 TCCTCTTTGAAAGCGGATTCGATTTATCAGCAACCAAAAGTGGCGGCTTAAACAA 1020  
QY 1021 GGCTGTTCCGAGCGGATTTTCCACTGACCGGCACTATATCAGAGGATTTTCGAG 1080  
Db 1021 GGCTGTTCCGAGCGGATTTTCCACTGACCGGCACTATATCAGAGGATTTTCGAG 1080  
QY 1081 AATATATACAAACCGCAGCATGGACACCCGATTCAAAGCTTTTACTTTGCGGTATGGACAGC 1140  
Db 1081 AATATATACAAACCGCAGCATGGACACCCGATTCAAAGCTTTTACTTTGCGGTATGGACAGC 1140  
QY 1141 CAACCGTTGCAACTGGGCGGCCCAACATCGCTTGTGCTTTAAACTTTTCGCCAGTCGCGCT 1200

Matches 2369; Conservative 0; Mismatches 9; Indels 0; Gaps 0;			
Qy	1	ATGAACCAATTACACATGCTTCTATTTCGCGCTGCTGGCAGTATTTTCGCAATCCG	60
Db	1	ATGAACCAATTACACATGCTTCTATTTCGCGCTGCTGGCAGTATTTTCGCAATCCG	60
Qy	61	GTCTTGGCAGCGGATGAAGCTGCAACCGGAAACACACCCGTTAAAGCAGAGATAAAGAA	120
Db	61	GTCTTGGCAGCGGATGAAGCTGCAACCGGAAACACACCCGTTAAAGCAGAGATAAAGAA	120
Qy	121	GTGCGGTTAAAGACAGCTTAATGCGCTGCAACCGTGAAGCTGCAACCTCGGCGC	180
Db	121	GTGCGGTTAAAGACAGCTTAATGCGCTGCAACCGTGAAGCTGCAACCTCGGCGC	180
Qy	181	ATTCAACAGCAATGATAGCGGCAACAAAGACTTGGTGTCTACCTCCACCGAGCTCGGC	240
Db	181	ATTCAACAGCAATGATAGCGGCAACAAAGACTTGGTGTCTACCTCCACCGAGCTCGGC	240
Qy	241	TTGAGCGATAGCGGCCCATCAAAAGGCTTTGCTGTGCGCGGTGGAAGGCAACCGT	300
Db	241	TTGAGCGATAGCGGCCCATCAAAAGGCTTTGCTGTGCGCGGTGGAAGGCAACCGT	300
Qy	301	GTGCGTGTGAGCGGTGAGCTGCTGATTCGGAAGAAACTCACTGTATGCA	360
Db	301	GTGCGTGTGAGCGGTGAGCTGCTGATTCGGAAGAAACTCACTGTATGCA	360
Qy	361	CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCGGAACCTCGTGGCGCAATC	420
Db	361	CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCGGAACCTCGTGGCGCAATC	420
Qy	421	GAAATCGGAAAGGCGCTGACTCTTTCAATACCGGTAGCGGCGCAATGGGTGGCGCGTG	480
Db	421	GAAATCGGAAAGGCGCTGACTCTTTCAATACCGGTAGCGGCGCAATGGGTGGCGCGTG	480
Qy	481	AATTACCAACCTGCAAGGACATGATTTGCTGTGGACGACAGGCAATTCGCGCTGATG	540
Db	481	AATTACCAACCTGCAAGGACATGATTTGCTGTGGACGACAGGCAATTCGCGCTGATG	540
Qy	541	ATGMAAACCGTTACAGCAGCGCAACCGGAATGACAAATACACTTCGGTTTCGGTGTG	600
Db	541	ATGMAAACCGTTACAGCAGCGCAACCGGAATGACAAATACACTTCGGTTTCGGTGTG	600
Qy	601	AGCAACGACCGGTGGATCCGCTTGTGTATTCGCAACGTCGCGGTCAAGACCGAA	660
Db	601	AGCAACGACCGGTGGATCCGCTTGTGTATTCGCAACGTCGCGGTCAAGACCGAA	660
Qy	661	AGGCGGGCGAGCTGGCTATCCGTTAGAGGTGCTGGCAGCGGCAATTCGCTGT	720
Db	661	AGGCGGGCGAGCTGGCTATCCGTTAGAGGTGCTGGCAGCGGCAATTCGCTGT	720
Qy	721	TGCTACGCGGTATCCCTGATCCGTCAACACAAATACCAACTTCTTGGGTAAAT	780
Db	721	TGCTACGCGGTATCCCTGATCCGTCAACACAAATACCAACTTCTTGGGTAAAT	780
Qy	781	GCTTATCAATCAACGACAGCAACCGATCGGCCATCGTTTAAACCGCGCAGCGGCGAT	840
Db	781	GCTTATCAATCAACGACAGCAACCGATCGGCCATCGTTTAAACCGCGCAGCGGCGAT	840
Qy	841	AATTACAGATGAAGAGCTTATACCTGACCGCTTCTTCTGGCGCGAAGCCGATGAC	900
Db	841	AATTACAGATGAAGAGCTTATACCTGACCGCTTCTTCTGGCGCGAAGCCGATGAC	900
Qy	901	GTAAACAGACGGCGCAATGCAACCTCTTTTACGAATGACGCTGATTCAAATTCGGCTG	960
Db	901	GTAAACAGACGGCGCAATGCAACCTCTTTTACGAATGACGCTGATTCAAATTCGGCTG	960
Qy	961	TGCTCTTTGAAGCGGACTTCGATTAATCAGACAAACCAAGTGGCGGTTTAAACAA	1020
Db	961	TGCTCTTTGAAGCGGACTTCGATTAATCAGACAAACCAAGTGGCGGTTTAAACAA	1020
Qy	1021	GGCTCGTCCGACGAGTATTCACCTGGAACCGCAACTATTAATCAGAAAGGATTTGGAG	1080
Db	1021	GGCTCGTCCGACGAGTATTCACCTGGAACCGCAACTATTAATCAGAAAGGATTTGGAG	1080

Qy	1081	AATATATCAACCGCAGCATGACACCCGATTCAAAAGTTTACTTTTGGTATGGACAGC	1140
Db	1081	AATATATCAACCGCAGCATGACACCCGATTCAAAAGTTTACTTTTGGTATGGACAGC	1140
Qy	1141	CAACCGTTGCAACTGGCGGCGCAACATCGTTGTGCTTTAAAGCTTTCCCGAGTCGGCT	1200
Db	1141	CAACCGTTGCAACTGGCGGCGCAACATCGTTGTGCTTTAAAGCTTTCCCGAGTCGGCT	1200
Qy	1201	GAGTTTGAAGACTTAAACCGGACGATTAATTAATTAATTAATTAATTAATTAATTAAT	1260
Db	1201	GAGTTTGAAGACTTAAACCGGACGATTAATTAATTAATTAATTAATTAATTAATTAAT	1260
Qy	1261	AGCTCGATTCAACACCCCGTGAAGAACCACTAATTAATTAATTAATTAATTAATTAAT	1320
Db	1261	AGCTCGATTCAACACCCCGTGAAGAACCACTAATTAATTAATTAATTAATTAATTAAT	1320
Qy	1321	CAATGAAGCAGCTGTTGACGAGCGGTGAGATATCCGTTAGCATCATACCAAAATGACG	1380
Db	1321	CAATGAAGCAGCTGTTGACGAGCGGTGAGATATCCGTTAGCATCATACCAAAATGACG	1380
Qy	1381	CCTCAGGAATGAATGCGGAGTGTATGCTTGTGACAAACACCGCTGCAGCAATACT	1440
Db	1381	CCTCAGGAATGAATGCGGAGTGTATGCTTGTGACAAACACCGCTGCAGCAATACT	1440
Qy	1441	TATAAGGCTGGAGCGGATTTGTCGGTTTGGCGGCGCAACTGAATCAGGCTTTGGCATGTC	1500
Db	1441	TATAAGGCTGGAGCGGATTTGTCGGTTTGGCGGCGCAACTGAATCAGGCTTTGGCATGTC	1500
Qy	1501	GCTTACGACATTAATTCGCGGTACCGGTGTCGCAATGCGTCCGAAAGTGTATTTCACTTAC	1560
Db	1501	GCTTACGACATTAATTCGCGGTACCGGTGTCGCAATGCGTCCGAAAGTGTATTTCACTTAC	1560
Qy	1561	AACCAAGTTCGGGTAAATTTGGCTGCCAATCCCAACCTGAAAGCGGAGCGACACAC	1620
Db	1561	AACCAAGTTCGGGTAAATTTGGCTGCCAATCCCAACCTGAAAGCGGAGCGACACAC	1620
Qy	1621	CACACCTGCTCTGCAAGGCGCGCAAGGAAAGGTAATTTGGATGCCAACCTGTATCAA	1680
Db	1621	CACACCTGCTCTGCAAGGCGCGCAAGGAAAGGTAATTTGGATGCCAACCTGTATCAA	1680
Qy	1681	AACAAATTCGCAACTTCTTGTCTGAAGAGAGAGTGTACCAACGCGGCGATGTCGCG	1740
Db	1681	AACAAATTCGCAACTTCTTGTCTGAAGAGAGAGTGTACCAACGCGGCGATGTCGCG	1740
Qy	1741	TGCTACTCAGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Db	1741	TGCTACTCAGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Qy	1801	TGGCAGATGCAAAATATCGATAAGGCGCGAAATCCGTTGGTCTTTGAGCTGACAGCGCTG	1860
Db	1801	TGGCAGATGCAAAATATCGATAAGGCGCGAAATCCGTTGGTCTTTGAGCTGACAGCGCTG	1860
Qy	1861	AATGTGACAAAGTGTAGCTTTTGTCTGAGGCTGGAATTTGTTCCGCTCGCTGGGT	1920
Db	1861	AATGTGACAAAGTGTAGCTTTTGTCTGAGGCTGGAATTTGTTCCGCTCGCTGGGT	1920
Qy	1921	TATGGAAGCAAACTGTGCGGCGCAACACGCTGCTCCACACAGCGCGCGGAAAGTG	1980
Db	1921	TATGGAAGCAAACTGTGCGGCGCAACACGCTGCTCCACACAGCGCGCGGAAAGTG	1980
Qy	1981	ATTGCGGTGTGCTACTGAGAAAGCGGCGGAAATTTGGGTGTGTTCTCCGCTGACT	2040
Db	1981	ATTGCGGTGTGCTACTGAGAAAGCGGCGGAAATTTGGGTGTGTTCTCCGCTGACT	2040
Qy	2041	TATCTGGGTGCAAAAGCGGCGCAATACACCGTTTATGAAACAAAGGCGCG	2100
Db	2041	TATCTGGGTGCAAAAGCGGCGCAATACACCGTTTATGAAACAAAGGCGCG	2100
Qy	2101	GGTACGCTTTTCAGAAAGGTAAGATTAACCGTGGCTGCAACAAAGTTCGCTTATG	2160
Db	2101	GGTACGCTTTTCAGAAAGGTAAGATTAACCGTGGCTGCAACAAAGTTCGCTTATG	2160



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OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 19:52:52 ; Search time 405 Seconds  
(without alignments)  
9607.570 Million cell updates/sec

Title: US-09-665-358-7

Perfect score: 2378

Sequence: 1 ATGAACCAATTACACATGCT.....GATTGGAAGTTTGAATTCC 2378

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2363.6	99.4	2378	3	US-08-817-707-7
2	2358.8	99.2	2378	3	US-08-537-361E-7
3	1930.2	83.7	3318	3	US-08-990-470A-1
4	1930.2	83.7	3318	3	US-08-817-707-1
5	1988.6	83.6	3318	1	US-08-326-670A-1
6	1985.4	83.5	3319	3	US-08-537-361E-1
7	1983.8	83.4	2379	3	US-08-537-361E-5
8	1958.4	82.4	2373	3	US-08-817-707-5
9	1849.6	77.8	2376	3	US-08-817-707-3
10	1848	77.7	2376	3	US-08-537-361E-3
11	68.4	2.9	1401	4	US-09-252-931A-14258
12	68.4	2.9	1767	4	US-09-252-931A-14416
13	68.4	2.9	3738	4	US-09-252-931A-14364
14	65.4	2.8	2809	3	US-08-448-194-5
15	65.4	2.8	2809	3	US-08-867-921-5
16	65	2.7	3286	2	US-08-363-124A-1
17	63.8	2.7	2955	2	US-08-867-941-9
18	63.8	2.7	2955	3	US-09-074-658-9
19	63.8	2.7	3000	2	US-08-867-941-8
20	63.8	2.7	3000	3	US-09-074-658-8
21	63.8	2.7	7641	2	US-08-867-941-6
22	63.8	2.7	7641	3	US-09-074-658-6
23	63.6	2.7	2370	4	US-09-252-931A-10440
24	62.2	2.6	3012	4	US-09-540-236-837
25	60.8	2.6	2826	3	US-08-624-655A-1
26	60.8	2.6	1830121	4	US-09-557-884-1
27	60.8	2.6	1830121	4	US-09-643-990A-1

28 60.6 2.5 49617 4 US-09-596-002-28 Sequence 28, Appli

29 59.4 2.5 2859 5 PCT-US96-05320A-637 Sequence 637, Appli

30 59.4 2.5 3252 3 US-08-476-102A-4 Sequence 4, Appli

31 59.4 2.5 3252 5 PCT-US96-05320A-714 Sequence 714, Appli

32 57.4 2.4 2955 2 US-08-867-941-4 Sequence 4, Appli

33 57.4 2.4 2955 3 US-09-074-658-4 Sequence 4, Appli

34 57.4 2.4 3000 2 US-08-867-941-3 Sequence 3, Appli

35 57.4 2.4 3000 3 US-09-074-658-3 Sequence 3, Appli

36 57.4 2.4 7650 2 US-08-867-941-1 Sequence 1, Appli

37 57.4 2.4 7650 3 US-09-074-658-1 Sequence 1, Appli

38 55.8 2.3 2696 1 US-07-961-522-1 Sequence 1, Appli

39 55.8 2.3 2696 1 US-08-217-438-1 Sequence 1, Appli

40 55.8 2.3 2696 1 US-08-321-978-1 Sequence 1, Appli

41 55.8 2.3 2696 2 US-08-710-584-1 Sequence 1, Appli

42 54.8 2.3 2800 3 US-08-448-194-3 Sequence 3, Appli

43 54.8 2.3 2800 3 US-08-867-921-3 Sequence 3, Appli

44 54.8 2.3 3537 2 US-08-363-124A-3 Sequence 3, Appli

45 54 2.3 2397 4 US-09-489-039A-2874 Sequence 2874, Ap

#### ALIGNMENTS

RESULT 1

US-08-817-707-7

; Sequence 7, Application US/08817707

; Patent No. 6277382

; GENERAL INFORMATION:

; APPLICANT: Stojiljkovic, Igor

; APPLICANT: So, Magdalena

; APPLICANT: Hwa, Vivian

; APPLICANT: Heffron, Fred

; APPLICANT: Nassif, Xavier

; TITLE OF INVENTION: No. 6277382a1 Bacterial Hemoglobin Receptor

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive, 32nd Floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/817,707

; FILING DATE: 19-AUG-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6277382naa, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 94,784-J

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-913-0001

; TELEFAX: 312-913-0002

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2378 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..2370

US-08-817-707-7

Query Match 99.4%; Score 2363.6; DB 3; Length 2378;

Best Local Similarity 99.6%; Pred. No. 0;





DR P-PSDB; ABP76975.  
XX  
PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a  
XX medicament for treating or preventing *N. gonorrhoeae* infection.  
XX  
XX Disclosure; Page 223; 815pp; English.  
XX  
CC The present invention relates to proteins from *Neisseria gonorrhoeae*.  
CC Also disclosed are the nucleic acid molecules encoding the proteins and  
CC antibodies that specifically bind to the proteins. The composition  
CC comprising the protein, nucleic acid or antibody is useful for the  
CC manufacture of a medicament for treating or preventing *N. gonorrhoeae*  
CC infection, this may be in the form of a vaccine or gene therapy.  
CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid  
CC molecules of the invention  
XX  
SQ Sequence 348 BP; 93 A; 87 C; 89 G; 79 T; 0 U; 0 Other;  
Query Match 14.5%; Score 344.8; DB 10; Length 348;  
Best Local Similarity 99.4%; Pred. No. 6.6e-96;  
Matches 346; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2023 GTGTTCTCCCGCTGACTTATCTGGTGCGAAAAAGGCCAAAGACGCGCAATACACCGTT 2082  
DB 1 GTGTTCTCCCGCTGACTTATCTGGTGCGAAAAAGGCCAAAGACGCGCAATACACCGTT 60  
QY 2083 TATGAACACAGGCGCGGTACCGCTTTCAGAAAGGTAAAGATTACCCCGTGCTG 2142  
DB 61 TATGAACACAGGCGCGGTACCGCTTTCAGAAAGGTAAAGATTACCCCGTGCTG 120  
QY 2143 AACAAAGTCGGCTATGTGTTGATGTATGACGGCTTCTACAACTGGCTTAAAACTGACT 2202  
DB 121 AACAAAGTCGGCTATGTGTTGATGTATGACGGCTTCTACAACTGGCTTAAAACTGACT 180  
QY 2203 TTGCGTCAGCGGTATATAATGTGTTCAACCGCAATAACACATTTGGGATTCCTCGCG 2262  
DB 181 TTGCGTCAGCGGTATATAATGTGTTCAACCGCAATAACACATTTGGGATTCCTCGCG 240  
QY 2263 GGTGTTGATAGCTACAGCACCACCAACGCGGTGCGACGAGATGCCAAGGCTTAGACCGC 2322  
DB 241 GGTGTTGATAGCTACAGCACCACCAACGCGGTGCGACGAGATGCCAAGGCTTAGACCGC 300  
QY 2323 TACCGCGCTCAGGCGGTAATTAAGCCGTATCGCTGGAATTTGAAAGTTT 2370  
DB 301 TACCGCGCTCAGGCGGTAATTAAGCCGTATCGCTGGAATTTGAAAGTTT 348  
RESULT 12  
ID ABZ37965 standard; DNA; 222 BP.  
XX  
AC ABZ37965;  
XX  
DT 07-MAR-2003 (first entry)  
XX  
DE *N. gonorrhoeae* nucleotide sequence SEQ ID 519.  
XX  
KW Antibacterial; infection; vaccine; gene therapy; gene; ds.  
XX  
OS *Neisseria gonorrhoeae*.  
XX  
PN WO200279243-A2.  
XX  
XX 10-OCT-2002.  
XX  
PF 12-FEB-2002; 2002WO-IB002069.  
XX  
PR 12-FEB-2001; 2001GB-00003424.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
XX Fontana MR, Pizza M, Masignani V, Monaci E;  
XX

DR WPI; 2003-058415/05.  
DR P-PSDB; ABP76995.  
XX  
PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a  
XX medicament for treating or preventing *N. gonorrhoeae* infection.  
XX  
XX Disclosure; Page 226; 815pp; English.  
XX  
CC The present invention relates to proteins from *Neisseria gonorrhoeae*.  
CC Also disclosed are the nucleic acid molecules encoding the proteins and  
CC antibodies that specifically bind to the proteins. The composition  
CC comprising the protein, nucleic acid or antibody is useful for the  
CC manufacture of a medicament for treating or preventing *N. gonorrhoeae*  
CC infection, this may be in the form of a vaccine or gene therapy.  
CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid  
CC molecules of the invention  
XX  
SQ Sequence 222 BP; 62 A; 54 C; 53 G; 53 T; 0 U; 0 Other;  
Query Match 8.4%; Score 199.4; DB 10; Length 222;  
Best Local Similarity 96.8%; Pred. No. 6.9e-51;  
Matches 214; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
QY 959 TGTGCTCTTTGAAGCGGACTTCGATTATCAGACACCAAGTGGCGGCTTAAACAACA 1018  
DB 2 TGTGCTCTTTGAAGCGGACTTCGATTATCAGACCAAAAGTGGCGGCTTAAACAACA 61  
QY 1019 AAGGCTGTTCCCGACGCGATTATTCACCTGGACGCGCAACTAT-AATCAGAAGGATTG 1077  
DB 62 AAGGCTGTTCCCGACGCGATTATTCACCTGGACGCGCAACTATATAATCAGAAGGATTG 121  
QY 1078 GAGAAATATACAAACCGCAGCATGGACACCCGATTCAAACGTTTACTTTTCGCTATGGAC 1137  
DB 122 GACCAATATACAAACCGCAGCATGGACACCCGATTCAAACGTTTACTTTTCGCTATGGAC 181  
QY 1138 AGCCAACCGTTGCAACTGGCGGCGCAACATCGCTTGTGCT 1178  
DB 182 AGCCAACCGTTGCAACTGGCGGCGCAACATCGCTTGTGCT 222  
RESULT 13  
ID AAA82041 standard; DNA; 558 BP.  
XX  
AC AAA82041;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE *N. meningitidis* partial DNA sequence gnm\_588 SEQ ID NO:588.  
XX  
KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; genome; immunogenic;  
XX antigen; vaccine; diagnosis; infection; antibacterial; identification;  
XX *Meningococcus B*; MenB; ds.  
XX  
OS *Neisseria meningitidis*.  
XX  
PN WO200022430-A2.  
XX  
PD 20-APR-2000.  
XX  
XX 08-OCT-1999; 99WO-US023573.  
XX  
PF 09-OCT-1998; 98US-0103794P.  
XX  
PR 30-APR-1999; 99US-0132068P.  
XX  
XX (CHIR) CHIRON CORP.  
XX  
PA Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
XX Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
XX Rappuoli R, Pizza M;  
XX WPI; 2000-318079/27.  
XX

QY 781 GCTTATCAATCAACGACACGACGATCGGCCATCGTCTTAAAGCCGACGAGGGGCAT 840  
 DB |||||  
 QY 781 GCTTATCAATCAACGACACGACGATCGGCCATCGTCTTAAAGCCGACGAGGGGCAT 840  
 DB |||||  
 QY 841 AATTACACGATT 852  
 DB |||||  
 QY 841 AATTACACGATT 852  
 DB |||||  
 RESULT 10  
 ABZ37953  
 ID ABZ37953 standard; DNA; 864 BP.  
 XX  
 AC ABZ37953;  
 XX  
 DT 07-MAR-2003 (first entry)  
 XX  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 495.  
 XX  
 KW Antibacterial; infection; vaccine; gene therapy; gene; ds.  
 XX  
 OS Neisseria gonorrhoeae.  
 XX  
 PN WO200279243-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 12-FEB-2002; 2002WO-IB002069.  
 XX  
 PR 12-FEB-2001; 2001GB-00003424.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 XX  
 PI Fontana MR, Pizza M, Massignani V, Monaci E;  
 XX  
 DR WPI; 2003-058415/05.  
 XX  
 PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
 XX  
 PS Disclosure; Page 224; 815pp; English.  
 CC  
 CC The present invention relates to proteins from Neisseria gonorrhoeae.  
 CC Also disclosed are the nucleic acid molecules encoding the proteins and  
 CC antibodies that specifically bind to the proteins. The composition  
 CC comprising the protein, nucleic acid or antibody is useful for the  
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
 CC infection, this may be in the form of a vaccine or gene therapy.  
 CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid  
 CC molecules of the invention  
 XX  
 SQ Sequence 864 BP; 228 A; 224 C; 209 G; 203 T; 0 U; 0 Other;  
 Query Match 35.1%; Score 833.8; DB 10; Length 864;  
 Best Local Similarity 98.5%; Pred. No. 1.8e-247;  
 Matches 852; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
 QY 1171 TTGTGCTTAAACCTTCCGAGTCGGCTGAGTTGAAACCTTAAACCGCAGCATAT 1230  
 DB 1 TTGTGCTTAAACCTTCCGAGTCGGCTGAGTTGAAACCTTAAACCGCAGCATAT 60  
 QY 1231 TACTTTCAGGGAAGAGTATCCGCTACTACAGCTCGATTCAACACCCGCTGAACCACT 1290  
 DB 1 TACTTTCAGGGAAGAGTATCCGCTACTACAGCTCGATTCAACACCCGCTGAACCACT 120  
 QY 1291 AATTATGTTTCTCACTGTCTGATCAAAATCCAAATGGAACGAGCTGTTCAGCAGCGTGCA 1350  
 DB 121 AATTATGTTTCTCACTGTCTGATCAAAATCCAAATGGAACGAGCTGTTCAGCAGCGTGCA 180  
 QY 1351 GATATCCGTTAGCATCATACCAAAATGACGCTCAGGAATGAATGCCAGTGTATGCT 1410  
 DB 181 GATATCCGTTAGCATCATACCAAAATGACGCTCAGGAATGAATGCCAGTGTATGCT 240

QY 1411 TGTGACAAAACACGCTCGAGCCAACTTATTAAGGCTGGAGCGGATTTCTCGGTTTG 1470  
 DB 241 TGTGACAAAACACGCTCGAGCCAACTTATTAAGGCTGGAGCGGATTTCTCGGTTTG 300  
 QY 1471 GCGGCGCAACTGAATCAGGCTTGGCATGTCGGTTACGACATTTCTCCGGCTACCGTGC 1530  
 DB 301 GCGGCGCAACTGAATCAGGCTTGGCATGTCGGTTACGACATTTCTCCGGCTACCGTGC 360  
 QY 1531 CCCAATGCTCGGAAGTGTATTTCACTTACAACGAGTTCGGGTAATTTGGCTGCCCAAT 1590  
 DB 361 CCCAATGCTCGGAAGTGTATTTCACTTACAACGAGTTCGGGTAATTTGGCTGCCCAAT 420  
 QY 1591 CCCAATGCTCGGAAGTGTATTTCACTTACAACGAGTTCGGGTAATTTGGCTGCCCAAT 1650  
 DB 421 TCCAACCTGGAAGCGGAGCGGAGCACCACCCCTGTCTCTGCAAGGCGCGAGCGAA 480  
 QY 1651 AAAGTACTTTGGATGCCAATCTGTATCAAAACAATTAACCGCAACTTCTTGTCTGAAGAG 1710  
 DB 481 AAAGTACTTTGGATGCCAATCTGTATCAAAACAATTAACCGCAACTTCTTGTCTGAAGAG 540  
 QY 1711 CAGAAGCTGACACGAGCGGAGTTCGGCTGTACTCAGATGAATTAATTAATTAATTAAT 1770  
 DB 541 CAGAAGCTGACACGAGCGGAGTTCGGCTGTACTCAGATGAATTAATTAATTAATTAAT 600  
 QY 1771 TGTAGCAATCTTATTCGAAACCCGGAATGGCAGATGCAAAATATCGATAAGGCCCGA 1830  
 DB 601 TGTAGCAATCTTATTCGAAACCCGGAATGGCAGATGCAAAATATCGATAAGGCCCGA 660  
 QY 1831 ATCCGTGCTTTGAGCTGACAGGCGCTCTGAAATGTGCAAAAGTAGCGTCTTTTGTCTCT 1890  
 DB 661 ATCCGTGCTTTGAGCTGACAGGCGCTCTGAAATGTGCAAAAGTAGCGTCTTTTGTCTCT 720  
 QY 1891 GAGGCTCGAAATTTCTCGGCTCGCTGAGTTATGCAAAAGCAAACTGTGCGGCGACAC 1950  
 DB 721 GAGGCTCGAAATTTCTCGGCTCGCTGAGTTATGCAAAAGCAAACTGTGCGGCGACAC 780  
 QY 1951 AGCTGCTGTCTCACACAGCGCCGAAAGTGTGCGGCTGCTGACTACGAAAGCCGAGC 2010  
 DB 781 AGCTGCTGTCTCACACAGCGCCGAAAGTGTGCGGCTGCTGACTACGAAAGCCGAGC 839  
 QY 2011 GAAAAATGGGTGTGTTCTCCGCGC 2035  
 DB 840 GAAAAATGGGTGTGTTCTCCGCGC 864  
 RESULT 11  
 ABZ37945  
 ID ABZ37945 standard; DNA; 348 BP.  
 XX  
 AC ABZ37945;  
 XX  
 DT 07-MAR-2003 (first entry)  
 XX  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 479.  
 XX  
 KW Antibacterial; infection; vaccine; gene therapy; gene; ds.  
 XX  
 OS Neisseria gonorrhoeae.  
 XX  
 PN WO200279243-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 12-FEB-2002; 2002WO-IB002069.  
 XX  
 PR 12-FEB-2001; 2001GB-00003424.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 XX  
 PI Fontana MR, Pizza M, Massignani V, Monaci E;  
 XX  
 DR WPI; 2003-058415/05.



PA (UYOR-) UNIV OREGON HEALTH SCI.  
 XX Stojiljkovic I, So M, Hwa V, Heffron P, Nassif X;  
 PI WPI; 1996-222006/22.  
 XX P-PSDB; AAR95566.  
 DR DNA encoding Neisseria haemoglobin receptor proteins - for use in  
 PT preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.  
 XX Claim 3; Page 52-55; 104pp; English.  
 PS A DNA sequence (AAT26998) codes for the bacterial haemoglobin receptor  
 XX (Hmbr) (AAR95566) of N. meningitidis serotype A. It was obtd. by PCR  
 CC amplification of genomic DNA using primers (AAT27001-02) based on the N.  
 CC meningitidis serotype C hmbR gene (see also AAT26997). The gene can be  
 CC used to prepare recombinant haemoglobin receptor protein, useful as a  
 CC vaccine for meningitis. It can be expressed in attenuated Salmonella host  
 CC cells. It can also be utilised as a probe to detect infection in humans.  
 CC hmbR genes for N. meningitidis serotype B (AAT26999) and for N.  
 CC gonorrhoeae (AAT27000) were similarly obtd. (Updated on 25-MAR-2003 to  
 CC correct PR field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated  
 CC on 27-AUG-2003 to correct OS field.)  
 XX Sequence 2376 BP; 632 A; 622 C; 621 G; 501 T; 0 U; 0 Other;  
 SQ

Query Match 77.6%; Score 1846.4; DB 2; Length 2376;  
 Best Local Similarity 86.4%; Pred. No. 0;  
 Matches 2052; Conservative 0; Mismatches 321; Indels 3; Gaps 1;

QY 1 ATGAAACCAATTACACATGTTCTTATTCGCGCTGCTGCGCAGTATTTTCGGCAATCCG 60  
 DB 1 ATGAAACCAATTACAAATGCCCTATTCGCGCGCTGCTGCGCAGTATTTTCGGCAATCCG 60  
 QY 61 GTCTTGGCAGCGGATGAAGCTGCAACCCGAAACACACCCGTTTAAAGCAGATTAAGA 120  
 DB 61 GTCTTGGCAGCGGATGAAGCTGCAACCCGAAACACACCCGTTTAAAGCAGATTAAGA 120  
 QY 121 GTGCGGTTTAAAGACCGAGCTTAATGCGCTGCAACCGTGAACCTCGGCCG 180  
 DB 121 GTGCGGTTTAAAGGTCAGGCGAATGCGCTGCGCTGGAACCGGTCAACCTTAACCGT 180  
 QY 181 ATCAACAGGAATGATACGCGACCAACAAAGACTTTGGTGGTTACTTCCACCGACGTGCGC 240  
 DB 181 ATCAACAGGAATGATACGCGACCAATAAAGACTTTGGTGGCTATTTCCACCGATGTCGCG 240  
 QY 241 TTGAGGATAGCGCGCCCATCAAAAGCTTTGCTGCGCGCGGTGGAAGGCAACCGT 300  
 DB 241 TTGAGCGACAGAGCGCGTCAATCAAAAGCTTTGCCATTCGCGCGGTGGAAGGCGACCGT 300  
 QY 301 GTCCGTTGTCAGATTGACGCGGTGAGCCTGCTGATTCGGAAGAAACTCACTGTATGCA 360  
 DB 301 GTCCGTTGATTGACGCGGTGAACCTGCTGATTCGGAAGAAACTCGCTGTACGCC 360  
 QY 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCGAACTCGTGGCGCAACATC 420  
 DB 361 CGTTATGGCAACTTCAACAGCTCGCGTGTCTATCGACCCCGAACTCGTGGCGCAACATC 420  
 QY 421 GAAATCGCAAGGCGCTGACTCTTTCAATACGCTAGCGCGGCAATGGGTGGCGCGGTG 480  
 DB 421 GACATCGTAAAGGCGGCGACTCTTTCAATACGCGCGGCGCTTGGCGCGCGGTG 480  
 QY 481 AATTACCAACCTCGCAAGGATGATTTGCTGTTGACGACAGGCAATTCGCGCTGATG 540  
 DB 481 AATTACCAACCTCGCAAGGATGATTTGCTGTTGCTGTTGACGCGGATTCGCGCTGATG 540  
 QY 541 ATGAAAAACGGTTACAGCAGCGCGCAACCGCAATGGAATAATACACTCGGTTTCGGTGTG 600  
 DB 541 ATGAAAAACGGTTACAGCAGCGGTAAACCGTGAATGGAATAATACACTCGGTTTCGGTGTG 600  
 QY 601 AGCAACGACCGGTGATCGCGCTTGTGTTATTCGCAACGTCGCGGTATCAGACCGAA 660  
 DB 601 AGCAACGACCGGTGATCGCGCTTGTGTTATTCGCAACGCGCGGCGCAATGAAACTGAA 660

QY 661 AGCGCGGCGAGCGTGGCTATCCGGTAGAGGGTGTGGCAGCGAGCAATATTCGGTGGT 720  
 DB 661 AGCGCGGCGAGCGTGGTATCCGGTAGAGGGTGTGGTAGCGGAGCAATATTCGGTGGT 720  
 QY 721 TCGTCACGCGGTATCCCTGATCCGTCGCAACAAATACCAACACTTCTTGGTGAAGATT 780  
 DB 721 TCTGCGCGGTATTCCTGATCCGTCGCAACAAATACCAACACTTCTTGGTGAAGATT 780  
 QY 781 GCTTATCAATCAACGACAGCACCGCATCGGCCCATCGTTTAAACGGCGACGAGGGCAT 840  
 DB 781 GCTTATCAATCAACGACAGCACCGCATCGGCCCATCGCTCAACGGTTCAGCAGGGCAT 840  
 QY 841 AATTACAGATTGAAGAGTCTTATACCTGACCGCTTCTTCTGCGCGCAAGCCGATGAC 900  
 DB 841 AATTACAGATTGAAGAGTCTTACAACTGCTTCTTCTTATTTGGCGTGAACCTGACGAT 900  
 QY 901 GFAAACAGACGCGCAATGCGCAACCTCTTTTACGAATGACGCGCTGATTCAAATTTGGCTG 960  
 DB 901 GTCAACAGACGCGGTAAACCAACCTCTTTTACGAATGACGCGCGAATCCGACCGGTG 960  
 QY 961 TCGTCTTTGAGGCGGACTTCGATTTATCAGACCAACCAAGTGGCGCGGTTAACACAA 1020  
 DB 961 TCTATGTTAAAGCGGATGTCGATTTATCAAAACCAAGATATCTGCGGTCAACTACAA 1020  
 QY 1021 GGCTCGTTCCGACCGGATTTATTCACCTGGACGCGCAACTATAATCAGAAGGATTTGGAG 1080  
 DB 1021 GGTTCGTTCCGACGAAATTTACACCATGGGAAACCGAGTACCATAAAGGAGTTGGC 1080  
 QY 1081 AATATATCAACCGCAGCATGGACACCGGATTCAAAGTTTAACTTTCTTTGCGTATGACACG 1140  
 DB 1081 GAAATCTATAACCGCAGCATGGATACAACTTCAAAACGTTATTAACGCTGCTGATGACACG 1140  
 QY 1141 CAACCGTTGCAACT---GGGCGGCCAACATCGTTCGCTTAAACCTTCCGCCGCTCGG 1197  
 DB 1141 CATCGTTGCAACTCGGGGGGGGGGACACCGCTGTCGTTCAAAACCTTTTCCCGGGCAG 1200  
 QY 1198 CTGAGTTTGAACAACTTAAACCGCGCAGATTTATTAATTCAGCGAAAGATATCCCGTACT 1257  
 DB 1201 CGTGATTTGAAACCTTAAACCGCGCAGATTTACTTACTTTCAGCGCGCGTGTTCGTAACC 1260  
 QY 1258 ACCAGCTCGATTCAACACCGCGTGAAACCACTAATATATGTTTCTCACTGCTGATCAA 1317  
 DB 1261 ACCAACAGTATCCAGCATCCGCTGAAACCACTAACTACGCTTCTCGCTGTCGACCAAA 1320  
 QY 1318 ATCCAATGMAACGAGCTGTCAGACGCGTCGAGATATCCGTTAGCATATACCAAAATG 1377  
 DB 1321 ATCCAATGMAACGAGCTGTCAGTAGCGCGAGGTATCCGTTACGACCAACCAAAATG 1380  
 QY 1378 ACGCTCAGGAATTCGAATGCGAGTGTATGCTGTCGACAAACACCGCTTCGACCAAT 1437  
 DB 1381 ACGCTCAGGAATTCGAATGCGAGTGTATGCTGTCGACAAACACCGCTTCGACCAAC 1440  
 QY 1438 ACTTATAAGGCTGAGCGGATTTGCTGCGGTGGCGCGCAACTGAATCAGGCTTGGCAT 1497  
 DB 1441 ACTTATAAGGCTGAGCGGATTTGCTGCGCTGGCGGCGAGCTGAGCAGCAACATGGCGT 1500  
 QY 1498 GTCGTTAGCAGCATTTACTTTCGCGTACCGTGTCCCAATCGTCCGAGTGTATTTCACT 1557  
 DB 1501 TTGGTTAGCATGTGACCTCAGGTTTCCGCTGCGCAATCGCTGGAAGTGTATTTCACT 1560  
 QY 1558 TACAACCAAGCTTCGGGTAAATTTGGCTGCGCAATCCCACTGAAAGCCGAGCGCAGCAC 1617  
 DB 1561 TACAACCAAGCTTCGGGCATTTGGAAGCTTAATCTTAATTTGAAGGCAACCGCTTCAGCACC 1620  
 QY 1618 ACCGACACCTGTCTCTGGAAGCGCGAGCAAAAGGTACTTTTGGATGCGCAACCTGTAT 1677  
 DB 1621 ACCGACACCTGTCTCTGAGGGCGCGCGCAAAAGGAGCACATGGATGCCAACCTGTAT 1680  
 QY 1678 CAARAACATTAACGCAACTTCTGTCAGAGAGAGAGCTGACCAACCGCGCGCATGTC 1737  
 DB 1681 CAARAACATTAACGCAACTTCTGTCGGAAGAGAGAGATCTGACTGTGAGCGGCAACCC 1740

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Db 601 AGTAACGACCGCTGGATCTGCTTTCTGCTATTTCGCAACGGCGCGCCATGAACCGAA 660
Qy 661 AGCGGGGCGAGCGTGGCTATCCGGTAGAGGGTCTCGCAGCGAGCAATATCCGTGGT 720
Db 661 AGCGGGGCGAACCGCGCTATCCGGTAGAGGGTCCGGTAAAGAAACGAATATCCGCGGT 720
Qy 721 TCGTACGCGGTATCCCTGTATCCGTCCAAACACAAATACCAAACTCTCTGGGTAAAGATT 780
Db 721 TCCGCGCGCGCATCCCGATCCGTCCAAACACAAATACCAAACTCTCTGGGTAAAGATT 780
Qy 781 GCTTATCAAAATCAACGACACCGCATCGGCCATCGTTTAAACGCGCAGCGAGGGCAT 840
Db 781 GCTTATCAAAATCAACGACACCGCATCGGCCATCGCTCAACGGTTCAGCAGGGGCAT 840
Qy 841 AATTACAGATTGAAGAGTCTTATAACCTGACCGCTCTTCTCGCGCGAAGCCGATGAC 900
Db 841 AATTACAGATTGAAGAGTCTTATAACCTGACCGCTCTTCTCGCGCGAAGCCGATGAC 900
Qy 901 GTAAACAGACGGCGCAATGCCAAGCTCTTTTACCAATGGAGCGCTGATTCAAAATGGCTG 960
Db 901 GTAAACAGACGGCGCAATGCCAAGCTCTTTTACCAATGGAGCGCTGATTCAAAATGGCTG 960
Qy 961 TCGTCTTTGAAGCGGACTTCGATTATCAGAAAACCAAAGTGGCGCGGATT---AACAAA 1017
Db 1021 GGCTCGTTCGCGAGGATTTCCACCTGGACGCGCACTATATCAGAAAGATTTCGAG 1080
Qy 1081 AATATATACAAACCGCAGATGACACCGGATTCAAAAGTTTACTTTTCGCGTATGACAGC 1140
Db 1078 GAAATATACAAACCGCAGATGACACCGGATTCAAAAGTTTACTTTTCGCGTATGACAGC 1137
Qy 1141 CAACCGTTGCAACT---GGGCGCGCAACATCGCTTGTGCTTAAACCTTCGCGCAGTCGG 1197
Db 1138 CATCGTTGCAACTCGCGGGGGGGCGACACCGCTGTCTGTTTAAACCTTCGCGCAGCGC 1197
Qy 1198 CGTGAGTTGGAATTAACCGGAGGATTTACTTTCAGGAAAGATTCCTCGCTACT 1257
Db 1198 CGTGAGTTGGAATTAACCGGAGGATTTACTTTCAGGAAAGATTCCTCGCTACT 1257
Qy 1258 ACCAGCTCGATTCAACACCCCGTCAAAACCACTAATTTATGTTTCTCACTGTCTGATCAA 1317
Db 1258 ACCAGCTCGATTCAACACCCCGTCAAAACCACTAATTTATGTTTCTCACTGTCTGATCAA 1317
Qy 1318 ATCAATGGAACGACGTGTTTCAGTAGCGCGCGAGTATCCGTTACGACCAACCAAAATG 1377
Db 1318 ATCAATGGAACGACGTGTTTCAGTAGCGCGCGAGTATCCGTTACGACCAACCAAAATG 1377
Qy 1378 ACGCTCAGGAATTAAGTCCGAGTGTCTGTCGAGCAAAACACCGCTCGAGCCAAT 1437
Db 1378 ACGCTCAGGAATTAAGTCCGAGTGTCTGTCGAGCAAAACACCGCTCGAGCCAAT 1437
Qy 1438 ACTTATAAGGCTCGAGCGGATTTGTCGGTTTGGCGGCGCAACTGAATCAGGCTTGGCAT 1497
Db 1438 ACTTATAAGGCTCGAGCGGATTTGTCGGTTTGGCGGCGCAACTGAATCAGGCTTGGCAT 1497
Qy 1498 GTCGGTTACGACATTAATTCGGGTACCGTGTCCCAATGCGTCCGAAGTGTATTTCACT 1557
Db 1498 GTCGGTTACGACATTAATTCGGGTACCGTGTCCCAATGCGTCCGAAGTGTATTTCACT 1557
Qy 1558 TACAACCAAGGCTCGGGAATTTGCTGCCAATCCCAACTGAAAGCGGAGCGAGCAC 1617
Db 1558 TACAACCAAGGCTCGGGAATTTGCTGCCAATCCCAACTGAAAGCGGAGCGAGCAC 1617
Qy 1618 ACCACACCTCTCTCTCAAGGCGCGAGCGAAAGGCTACTTTGGATGCCAACCTGTAT 1677
Db 1618 ACCACACCTCTCTCTCAAGGCGCGAGCGAAAGGCTACTTTGGATGCCAACCTGTAT 1677
Qy 1678 CAACACATTAACCGCACTTCTGTCGAGAGCAGAGCTGACCAACGAGGCGATGTC 1737
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Db 1678 CAACGCAATTAACCGCAATTTCTGTTCTGAAGAGCAGAAGCTGACACCGAGCGCACTCC 1737
Qy 1738 GGCTGTACTCAGATGAATTAATACTACTAGGTATGTGTAGCAATCTTATTCGAAAAACCG 1797
Db 1738 GGCTGTACTCAGGAAATGCTTACTACAGTATATGACGACCCCTTACAAAGAAAACTG 1797
Qy 1798 GAATGGCAGATGCAAAATATCGATAGGCCCGAATCCGTGCTCTTGTAGCTGACAGGCGGT 1857
Db 1798 GAATGGCAGATGCAAAATATCGATAGGCCCGAATCCGTGCTCTTGTAGCTGACAGGCGGT 1857
Qy 1858 CTGAATGTGACAAAGTAGCGTCTTTTGTCTGAGGGCTGGAAAATTTGTCGGCTCGCTG 1917
Db 1858 CTGAATGTGACAAAGTAGCGTCTTTTGTCTGAGGGCTGGAAAATTTGTCGGCTCGCTG 1917
Qy 1918 GGTATGCGAAAAGCAAACTGTCGGCGCAACAGAGCTGCTGTCACACAGCGCGCGAAA 1977
Db 1918 GGTATGCGAAAAGCAAACTGTCGGCGCAACAGAGCTGCTGTCACACAGCGCGCTGAAA 1977
Qy 1978 GTGATTGCGCGGTTCGACTACGAAAGCCCGAGCGAAAATGGGGTGTGTTCTCCCGCTG 2037
Db 1978 GTGATTGCGCGGTTCGACTACGAAAGCCCGAGCGAAAATGGGGTGTGTTCTCCCGCTG 2037
Qy 2038 ACTTATCTGGGTGGAAGGCGCAAGAGCGCGCAATACACCGTTTATGAAAAACAGGCG 2097
Db 2038 ACTTATCTGGGTGGAAGGCGCAAGAGCGCGCAATACACCGTTTATGAAAAACAGGCG 2097
Qy 2098 CGGGGTACGCTTTGCAAGAAAAAGGTAAAGATTACCCGCTGGCTGAAACAAAGTCGGCTTAT 2157
Db 2098 TGGGTACGCTTTGCAAGAAAAAGGTAAAGATTACCCGCTGGCTGAAACAAAGTCGGCTTAT 2157
Qy 2158 GTGTTGATATGATACCGCTTCTACAACTGCGCTTAAACCTGACTTTTGTGAGGCGTA 2217
Db 2158 GTGTTGATATGATACCGCTTCTACAACTGCGCTTAAACCTGACTTTTGTGAGGCGTA 2217
Qy 2218 TATAATGTGTTCAACCGCAATACCACTTGGGATTCCTGCGCGGTTTGTATAGCTAC 2277
Db 2218 TACAACCTGTTTCAACCGCAATACCACTTGGGATTCCTGCGCGGTTTGTATAGCTAC 2277
Qy 2278 AGCACCAACCAACCGGTTCGACCGAGATGCAAGGCTTAGACCGCTACCGCGCTCAGGC 2337
Db 2278 AGCACCAACCAACCGGTTCGACCGAGATGCAAGGCTTAGATCGCTACCGCGCCAGGC 2337
Qy 2338 CGTAATTAACCGCTGATCGCTGGAATTTGA 2373
Db 2338 CGCAATTAACCGCTGATCGCTGGAATTTGA 2373

RESULT 8
AAT26998
ID AAT26998 standard; cDNA; 2376 BP.
XX
AC AAT26998;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-AUG-1996 (first entry)
XX
DE N. meningitidis serotype A haemoglobin receptor cDNA.
XX
KW Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; meningitis; ss.
XX
OS Neisseria meningitidis serogroup A.
XX
PN WO9612020-A2.
XX
PD 25-APR-1996.
XX
PF 17-OCT-1995; 95WO-US013623.
XX
PR 18-OCT-1994; 94US-00326670.
PR 02-OCT-1995; 95US-00537361.
XX
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Db 1681 TATCAAGCAATATCCGCAATTTCTGCTGAAGAGCAGAAGCTGACCACCGAGCGCGAT 1740  
 Qy 1735 GTCCGCTGTACTCAGATGAATTAAGTACTAGTGTGTAGCAATCTTATTCGGAAAAA 1794  
 Db 1741 GTGAGCTGTACTCAGATGAATTAAGTACTAGTGTGTAGCAATCTTATTCGGAAAAA 1800  
 Qy 1795 CCGGAATGCGAGATGCAAAATATCGATAGGCGCCGAATCCGTGGTCTTGAGCTGACAGCG 1854  
 Db 1801 CTGGAATGCGAGATGCAAAATATCGCAAGGCCAGATCCGGGTATCGAGCTGACGGCG 1860  
 Qy 1855 CGTCTGAATGTGACAAAAGTAGCGTCTTTTGTCTGAGGGCTGGAATGTTGGGCTCG 1914  
 Db 1861 CGTCTGAATGTGACAAAAGTAGCGTCTTTTGTCTGAGGGCTGGAATGTTGGGCTCG 1920  
 Qy 1915 CTGGGTATGCGAAAGCAAACTGTGCGGCGCAACAGAGCTGCTGCCACAGCGCGCG 1974  
 Db 1921 CTGGGTATGCGAAAGCAAACTGTGCGGCGCAACAGAGCTGCTGCCACAGCGCGTG 1980  
 Qy 1975 AAAGTGATTTGCGGTGTCGACTACGAAAGCCGAGCGGAAAAATGGGGTGTGTTCTCCGCG 2034  
 Db 1981 AAAGTGATTTGCGGTGTCGACTATGAAAGTCCGAGCGGAAAAATGGGGTGTGTTCTCCGCG 2040  
 Qy 2035 CTGACTTATCTGGGTGCGAAAAAGGCCAAAGACGCGCAATACACCGTTTATGAAACACAG 2094  
 Db 2041 CTGACCTATCTGGGCGCGAAAAAGGTCAAAGACGCGCAATACACCGTTTATGAAACACAG 2100  
 Qy 2095 GCGCGGGTACGCGCTTTGCGAAAAAGGTAAAGATTACCGTGGCTGAACAGTCGGCT 2154  
 Db 2101 GCGTGGGTACGCGCTTTGCGAAAAAGGTAAAGATTACCGTGGCTGAACAGTCGGCT 2160  
 Qy 2155 TATGTGTTTGATATGTACGGCTCTTACAACTGGCTTAAAGCTGACTTTGGCTGCGAGCG 2214  
 Db 2161 TATGTGTTTGATATGTACGGCTCTTACAACTGGCTTAAAGCTGACTTTGGCTGCGAGCG 2220  
 Qy 2215 GTATATATGTGTCAACGCGAAATACACCACTTGGGATTTCCCTGCGCGGTTGTATAGC 2274  
 Db 2221 GTATATATGTGTCAACGCGAAATACACCACTTGGGATTTCCCTGCGCGGCTGTATAGC 2280  
 Qy 2275 TACAGACCAACCAACGCGTTCGACCGAGATGCAAGGCTTAGACCGCTACCGCGCGCTCA 2334  
 Db 2281 TACAGACCAACCAACGCGTTCGACCGAGATGCAAGGCTTAGACCGCTACCGCGCGCTCA 2340  
 Qy 2335 GCGCGTAATTAGCGCTATCGCTGGAATGGAAGTTTGA 2373  
 Db 2341 AGCGGTAATTAGCGCTATCGCTGGAATGGAAGTTTGA 2379

## RESULT 7

AAT26997

AAT26997 standard; cDNA; 2373 BP.

AC AAT26997;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-AUG-1996 (first entry)

DE N. meningitidis serotype C haemoglobin receptor cDNA.

XX Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; meningitis;

KW 88.

XX Neisseria meningitidis serogroup C.

XX WO9612020-A2.

PN 25-APR-1996.

XX 17-OCT-1995; 95WO-US013623.

XX 18-OCT-1994; 94US-00326670.

PR 02-OCT-1995; 95US-00537361.

(UYOR-) UNIV OREGON HEALTH SCI.

XX Stojiljkovic I, So M, Hwa V, Heffron P, Nassif X;

XX WPI; 1996-222006/22.

DR P-PSDB; AAR95565.

XX DNA encoding Neisseria haemoglobin receptor proteins - for use in

XX preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.

XX Claim 2; Page 46-47; 104pp; English.

XX A DNA sequence (AAT26997) codes for the bacterial haemoglobin receptor

XX (HmbR) (AAR95565) of N. meningitidis serotype C isolate 8013 clone 6. It

XX was isolated from a cosmid library by auxotroph complementation cloning

XX and restriction enzyme digestion mapping of hemin utilisation positive

XX cosmids. A 3.3 kb DNA fragment including the hmbR open reading frame was

XX identified. The hmbR gene can be used to prepare recombinant receptor

XX protein, useful as a vaccine for meningitis. It can be expressed in

XX attenuated Salmonella host cells. It can also be utilised as a probe to

XX detect infection in humans. Genes for N. meningitidis serotypes A and B

XX and for N. gonorrhoeae were also obt'd. (see also AAT26998-T27000).

XX (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to

XX correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 2373 BP; 636 A; 627 C; 610 G; 500 T; 0 U; 0 Other;

XX Query Match 83.2%; Score 1979.2; DB 2; Length 2373;

XX Best Local Similarity 90.2%; Pred. No. 0;

XX Matches 2142; Conservative 0; Mismatches 228; Indels 6; Gaps 2;

Qy 1 ATGAACCATTAACATGCTTCTTATTCGCGCGTGTGTCGGCAGTATTTTCGGCAATCGG 60

Db 1 ATGAACCATTAACATGCTTCTTATTCGCGCGTGTGTCGGCAGTATTTTCGGCAATCGG 60

Qy 61 GTCTTGGCAGCAGATGAAGTGCACACTGAAACCAACACCGCTTAAAGCAGAGATAAAGAA 120

Db 61 GTCTTGGCAGCAGATGAAGTGCACACTGAAACCAACACCGCTTAAAGCAGAGATAAAGAA 120

Qy 121 GTGCGCGTTAAAGCAGCAGTAAATGCGGCTCAACCGTGGACGCTCAACCTCGGCGCG 180

Db 121 GTGCGCGTTAAAGCAGCAGTAAATGCGGCTCAACCGTGGACGCTCAACCTCGGCGCG 180

Qy 181 ATTCAACAGGAAATGATACGGCACAACAAAGACTTTGGTGCCTTACTCCACCGACGTCGGC 240

Db 181 ATTCAACAGGAAATGATACGGCACAACAAAGACTTTGGTGCCTTACTCCACCGACGTCGGC 240

Qy 241 TTGAGCGATAGCGCGCGCATCAAAAAGCTTTGTCTGTGCGCGCGGTGGAAGCGCAACCGT 300

Db 241 TTGAGCGATAGCGCGCGCATCAAAAAGCTTTGTCTGTGCGCGCGGTGGAAGCGCAACCGT 300

Qy 301 GTGCGGTGCAGATTTGACGGGTGAGCTGCTGATTCGGAGAGAAACTCAGCTGTATGCA 360

Db 301 GTGCGGTGCAGATTTGACGGGTGAGCTGCTGATTCGGAGAGAAACTCAGCTGTATGCA 360

Qy 361 CGTTATGGCACTTCAACAGCTCGCGCTGTCTATCGACCCCGCAACTCGTGCACACATC 420

Db 361 CGTTATGGCACTTCAACAGCTCGCGCTGTCTATCGACCCCGCAACTCGTGCACACATC 420

Qy 421 GAAATCGGAAGGGCGCTGACCTTTTCAATACCGGTAGCGGCGCATTTGGTGGCGCGGTG 480

Db 421 GAAATCGGAAGGGCGCTGACCTTTTCAATACCGGTAGCGGCGCATTTGGTGGCGCGGTG 480

Qy 481 AATTACCAAAACCTCGAAGGACATGATTTGCTGTTGGACGACGACGCAATTCGCGCGGTG 540

Db 481 AATTACCAAAACCTCGAAGGACATGATTTGCTGTTGGACGACGACGCAATTCGCGCGGTG 540

Qy 541 ATGAAAAACGGTTACAGCAGCGCAACCGCGAATCGCAAAATACACATACCTCGTTTCGGTGTG 600

Db 541 ATGAAAAACGGTTACAGCAGCGCGTAACCGTGAATGCAATACCTCGTTTCGGTGTG 600

Qy 601 AGCAACGACCGCGTGGATGCGCGCTTTGTGTATTTCGCAACGTCGCGGTTCATGAGACCGAA 660



PR	18-OCT-1994;	94US-00326670.
PR	02-OCT-1995;	95US-00537361.
XX	(UYOR-) UNIV OREGON HEALTH SCI.	
PA		
XX	Stojiljkovic I, So M, Hwa V, Heffron F, Nasaisif X;	
PI		
XX	WPI; 1996-222006/22.	
DR	p-PSDB; AAR95567.	
XX	DNA encoding Neisseria haemoglobin receptor proteins - for use in preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.	
PT	Claim 4; Page 58-61; 104pp; English.	
XX		
PS	A DNA sequence (AAT26999) codes for the bacterial haemoglobin receptor (Hmbr) (AAR95567) of N. meningitidis serotype B. It was obt'd. by PCR amplification of genomic DNA using primers (AAT27003-04) based on the N. meningitidis serotype C hmbR gene (see also AAT26997). The gene can be used to prepare recombinant haemoglobin receptor protein, useful as a vaccine for meningitis. It can be expressed in attenuated Salmonella host cells. It can also be utilised as a probe to detect infection in humans. CC hmbR genes for N. meningitidis serotype A (AAT26998) and for N. gonorrhoeae (AAT27000) were similarly obt'd. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)	
XX	Sequence 2379 BP; 621 A; 632 C; 611 G; 515 T; 0 U; 0 Other;	
SQ		
Query Match	83.6%; Score 1988.6; DB 2; Length 2379;	
Best Local Similarity	90.3%; Pred. No. 0;	
Matches 2149; Conservative	0; Mismatches 224; Indels 6; Gaps 2;	
Qy'	1 ATGAACCAATTACAGTCTTCTATGCGCGCTGGTCGGCAGTATTTTCGGCAATCCG 60	
Db		
1	ATGAACCAATTACAAATGTCTCCATPFCGCCGCCTGGTCGGCAGTATTTTCGGCAATCCG 60	
Qy	61 GTCTTGCGAGCGATGAAGCTGCAACCGAAACACACCCTGTTAAAGCAGAGATAAAGAA 120	
Db		
61	GTCTTTGCGCAGATGAAGCTGCAACTGAACACAACCCTTTAGCGAGAGTAAGAACA 120	
Qy	121 GTGCGGTTAAAGAACAGCTTAATGCGCTGCAACCGTGGAAAGCTGCAACCTCGCGCGC 180	
Db		
121	GTGCGGTTAAAGAACAGCTGCAATGCGCTGCGGCTGTGGAACGGCTCAACCTTAAACCGT 180	
Qy	181 ATTCAACAGGAATGATACGCGACCAAGACTTGGTCGCTTACTCCACGACGTGGGC 240	
Db		
181	ATCAAAACAAGAAATGATACGCGACCAAGAACTTGGTCGCTATTTCCACCGATGTGGGC 240	
Qy	241 TTGAGCGATAGCGCGCCCATCAAAAAGCTTTGCTGCGCGCGGTGGAAGGCAACCGT 300	
Db		
241	TTGAGCGACAGCGCGCCCATCAAAAAGCTTTGCTGCGCGCGGTGGAAGGCAACCGT 300	
Qy	301 GTGCGGTGTCAGCAATTGACGCGCTGAGCCTGCTGATTCGGAAAGAAAACTCACTGATGCA 360	
Db		
301	GTGCGGTGAGCATAGACGCGGTAAACCTGCTGATTTCCGAAGAAAACTGCTGTACGCC 360	
Qy	361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCAGAACTGTGGCGCAATC 420	
Db		
361	CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCAGAACTGTGTGGCGCAATC 420	
Qy	421 GAATCGCAAGGCGCTGACTCTTTCAATACCGTAGCGCGCAATTTGGGTGGCGCGTG 480	
Db		
421	GACATCGTAAAGGGCGGACTCTTTCAATACCGTAGCGCGCGCTTTGGGCGCGGTGTG 480	
Qy	481 AATTACCAAAACCTCGCAAGGACATGATTTGCTGTTGGACGACAGGCAATTCGGCGTGATG 540	
Db		
481	AATTACCAAAACCTCGCAAGGACGTACTTACTGTTGCCTGAACGCGAGTTTCGGCGTGATG 540	
Qy	541 ATGA AAAACCGTTTACAGAGCGCGCAACCGCGAATGACAATACTCGGTTTTGGGTGTG 600	
Db		
541	ATGA AAAACCGTTTACAGCAACCGCTTAACCGTGAATGACAATACTCGGTTTTTCGGCGTG 600	

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Db 242056 ATGAAAAACGGTTACAGCAGCGGTAAACCGTGAATGGAACAAATACTCTCGGTTTCGGTGTG 241997
Qy 601 AGCAACGCGCGTGGATCGCGCTTTCGTGTAATTCGACAGTTCGCGGTTCATCAGACCGNA 660
Db 241996 AGTAACGACGCGGTGGATGCTCTTTCGTGTAATTCGACAGTTCGCGGTTCATGAAACCGNA 241937
Qy 661 AGCGGGGCGAGCGGTGGCTATCCGGTAGAGGTGCTGGCAGCGAGCAATTAATTCGGTGT 720
Db 241936 AGTGGCGGNAACCGAGGCTATGCTGGGAAGGAGGAGTGGCGGATATCCGTGT 241877
Qy 721 TCGTCAACGCGGTATCCCTGATCCGTGCAAAACAAATACCAACATCTTCGGTGAAGATT 780
Db 241876 TCGGACGCGGTATCCCTGATTCGTGCAAAACAAATACCAACATCTTCGGTGAAGATT 241817
Qy 781 GCTTATCAATCAACGACAGCAGCAGCATCGGCCATCGTTTAAAGCGCAGCAGGGCAT 840
Db 241816 GCTTACCAATTAACGATTAACCAACCGCATCGCGCATCGCTTAAAGCGCAGCAGGGACAT 241757
Qy 841 AATTACACGATTGAAGAGTCTTATACCTGACCGCTTCTTCTGGCGCAAGCCGATGAC 900
Db 241756 AATTACACGATTGAAGAGTCTTATACCTGACCGCTTCTTCTGGCGCAAGCCGATGAC 241697
Qy 901 GTAACAGACGCGCAATGCCAATCTTTTACGAATGACGCGCTGATTCAAATTTGGCTG 960
Db 241696 GTAACAGACGCGCAATGCCAATCTTTTACGAATGACGCGCTGATTCAAATTTGGCTG 241637
Qy 961 TCGTCTTTGAAGCGGACTTCGATTATCAGACACCAAGTGGCGGTTAACACAA 1020
Db 241636 TCGTCTTTGAAGCGGACTTCGATTATCAGACACCAAGTGGCGGTTAACACAA 241577
Qy 1021 GCCTGCTTCCGACGATTAATCCACTGGACGCGCAATATAATCAGAAGATTGGAG 1080
Db 241576 GCCTGCTTCCGACGATTAATCCACTGGACGCGCAATATAATCAGAAGATTGGAG 241517
Qy 1081 AATATATCAACCGCAGATGACACCGCATTAACAGTTTACCTTGGTATGACACAG 1140
Db 241516 GAAATATCAACCGCAGATGACACCGCATTAACAGTTTACCTTGGTATGACACAG 241457
Qy 1141 CAACGCTTCAACT--GGGCGGCAACATCGCTTGTGCTTAAACTTTCCCGAGTCGG 1197
Db 241456 CATCGCTTCAACTCGGGGGGGGGGACACCGCTTGTGCTTAAACTTTCCCGAGTCGG 241397
Qy 1198 COTGAGTTTGAACCTTAAACCGCAGATTAATTAATTCAGCGAAGATATCCCGTACT 1257
Db 241396 COTGAGTTTGAACCTTAAACCGCAGATTAATTAATTCAGCGGCGTGTGTTGTCGAAC 241337
Qy 1258 ACCAGTCTGATTCACACCGCTGAAACCACTAATATGTTTCTCACTGCTGATCA 1317
Db 241336 ACCAGCAGTATCCAGCATCCGCTGAAACCACTAATATGTTTCTCACTGCTGACCAA 241277
Qy 1318 ATCCAATGAAACGAGTGTTCAGCAGCGCTGAGATATCCGTTAGCATATACCAAAATG 1377
Db 241276 ATTCAATGAAACGAGTGTTCAGTACCGCGGAGGATTCGTTACGACACCAAAATG 241217
Qy 1378 AGCCTCAGGAATGAATCCGAGTGTCTATGTTGTGACAAACACCGCTTCAGCCCAAT 1437
Db 241216 AGCCTCAGGAATGAATCCGAGTGTCTATGTTGTGACAAACACCACTTCAGCCCAAT 241157
Qy 1438 ACTTATAAGGCTGGAGCGGATTTGCTGGTTGGCGGCGCACTGAATCAGGCTTGGCAT 1497
Db 241156 ACTTATAAGGCTGGAGCGGATTTGCTGGCTTTGGCGGCGCACTGAATCAGGCTTGGCAT 241097
Qy 1498 GTCGGTTACGATTAATTCGCGCTACCGTTCCTCAATGCTGCGAGTGTATTCAT 1557
Db 241096 GTCGGTTACGATTAATTCGCGCTACCGTTCCTCAATGCTGCGAGTGTATTCAT 241037
Qy 1558 TACAACACGCTTGGGTAATTTGGTTCGCCAATCCCAACTGAAAGCCGAGCGCAGCAC 1617
Db 241036 TACAACACGCTTGGGTAATTTGGTTCGCCAATCCCAACTGAAAGCCGAGCGCAGCAC 240977
Qy 1618 ACCACACCTGTCTTCAGAGCGCGCAGGAAAGAGTACTTTGATGCCAACCTGTAT 1677
Db 240976 ACCACACCTGTCTTCAGAGCGCGCAGGAAAGAGTACTTTGATGCCAACCTGTAT 240917
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## RESULT 6

AAT26999

ID AAT26999 standard; cDNA; 2379 BP.

XX AAT26999;

AC AC

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-AUG-1996 (first entry)

XX XX

DE N. meningitidis serotype B haemoglobin receptor cDNA.

XX XX

KW Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; meningitis;

XX 88.

XX Neisseria meningitidis serogroup B.

XX WO9612020-A2.

XX 25-APR-1996.

XX 17-OCT-1995; 95WO-US013623.

XX XX

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Db      5567 GATTGGCAGATGAATAATATCGACAGGCCAGATCCGCGGTATCGAGCTGACAGCCGT 5508
Qy      1858 CTGAATGTGACAAAGTAGCGTCTTTTTCCTGAGGGCTGGAAATGTTTCGCTCGCTG 1917
Db      5507 CTGAATGTGACAAAGTAGCGTCTTTTTCCTGAGGGTGGAAATGTTTCGCTCGCTG 5448
Qy      1918 GGTATGCGAAAGCAACAGTCTGGGCGACACAGCTGCTGCTCCACAGCCGCCGAA 1977
Db      5447 GGTATGCGAAAGCAACAGTCTGGGCGACACAGCTGCTGCTCCACAGCCGCCGAA 5388
Qy      1978 GTGATTCGCGGTTCGCACTACGAAAGCCGAGCGGAAATGGGGTGTGTTCTCCCGCTG 2037
Db      5387 GTGATTCGCGGTTCGCACTACGAAAGTCCGAGCGGAAATGGGGTGTGTTCTCCCGCTG 5328
Qy      2038 ACTTATCTGGTGCAGAAAGGCCAAGACGCGCAATACACCGTTTATGAAAAAAGGGC 2097
Db      5327 ACTTATCTAGCGCGGAAAGGTCAGAGCGCGCAATACACCGTTTATGAAAAAAGGGC 5268
Qy      2098 CGGGGTACGCTTTGCAGAAAGGTAAGATTTACCGTGGCTGACAGTCCGCTTAT 2157
Db      5267 TGGGGTACGCTTTGCAGAAAGGTAAGATTTACCGTGGCTGACAGTCCGCTTAT 5208
Qy      2158 GTGTTTATGATGTACGGCTTCTCAAACTGGCTAAAAACCTGCTTTCGCTGACGGCGTA 2217
Db      5207 GTGTTTATGATGTACGGCTTCTCAAACTGGCTAAAAACCTGCTTTCGCTGACGGCGTG 5148
Qy      2218 TATAATGTGTTCAACCGCAATACACCACTTGGGATTCCTCGCGGTTTGTATAGCTAC 2277
Db      5147 TACAACCTGTTCACCGCAATACACCACTTGGGATTCCTCGCGGTTTATATAGCTAC 5088
Qy      2278 AGCACCAACCGGTCGACGAGATGGCAAGGCTTAGACCGCTACCGGCTCAGGC 2337
Db      5087 AGCACCAACCGGTCGACGAGATGGCAAGGCTTAGACCGCTACCGGCTCAGGC 5028
Qy      2338 CGTAATTAACCGCTATCGCTGGATTTGAAGTTTGA 2373
Db      5027 CGCAATTAACCGCTATCGCTGGATTTGAAGTTTGA 4992

RESULT 5
AAF21611/c
ID      AAF21611 standard; DNA; 349980 BP.
AC      AAF21611;
XX      13-MAR-2001 (first entry)
DT      Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
DE      Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW      diagnosis; antigen; detection; infection; gene therapy; antibacterial;
KW      ds.
XX      Neisseria meningitidis.
OS      WO20066791-A1.
XX      09-NOV-2000.
XX      08-MAR-2000; 2000WO-US005928.
XX      30-APR-1999; 99US-0132068P.
XX      08-OCT-1999; 99WO-US023573.
XX      28-FEB-2000; 2000GB-00004695.
XX      (CHIR ) CHIRON CORP.
XX      (GENO-) INST GENOMIC RES.
XX      Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;
XX      Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
XX      Rappuoli R, Frazer CM, Grandi G;

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DR      WPI; 2000-647603/62.
XX      Neisseria meningitidis B full length genome sequence and open reading
PT      frames are used to detect, treat and prevent Neisserial infections.
XX      Claim 7; Appendix A; 692pp; English.
XX      The present invention describes the full length genome of Neisseria
CC      meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC      represent fragments of the NMB genomic sequence, as the sequences which
CC      long to go in a record on its own it was split into 8 sequences which
CC      overlap each other at the beginning and end of each sequence by 49980 bp
CC      (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC      AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC      AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC      given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC      primers which are used in the exemplification of the present invention.
CC      The NMB genome and fragments from it have antibacterial activity, and can
CC      be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC      and/or antibodies which binds to the proteins can be used in compositions
CC      for treating or preventing infection due to Neisserial bacteria or as a
CC      diagnostic reagent for detecting the presence of Neisserial bacteria or
CC      of antibodies raised to Neisserial bacteria. Computers, computer memory,
CC      computer storage medium or computer databases can be used in a search to
CC      identify open reading frames (ORFs) or coding sequences within the NMB
CC      genome. The DNA sequences provide further opportunities to find antigenic
CC      or immunogenic proteins which are more effective in vaccines than the
CC      outer membrane proteins currently used
XX      SQ      Sequence 349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 U; 0 Other;
Query Match      85.7%; Score 2038.4; DB 3; Length 349980;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 2172; Conservative 0; Mismatches 201; Indels 3; Gaps 1;
Qy      1 ATGAAACCAATTACATGCTTCTATTTGCGCGCTGCTGGCAGTATTTTCGGCAATCCG 60
Db      242596 ATGAAACCAATTACAAATGCTCCCTATCGCGCGCTGCGCAGTATTTTCGGCAATCCG 242537
Qy      61 GTCTTCGCGAGCGATGAGCTGCAACCGCAACACACCCGTTTAAACGACAGATATAAGAA 120
Db      242536 GTCTTCGCGAGCGATGAGCTGCAACCGCAACACACCCGTTTAAACGACAGATATAAGAA 242477
Qy      121 GTGCGGCTTAAAGACACGAGCTTAAATGCGCGCTGCAACCGTGGAAACGCTGTCAACCTCGCGCG 180
Db      242476 GTGCGGCTTAAAGGTGAGCGCAATGCGCTGCGGCTGTGAAACGCTCAACCTTAACCGT 242417
Qy      181 ATTCAACAGGAATGATAGCGCAACAAAGACTTGTGCGCTTACTCCACCGAGCTCGGC 240
Db      242416 ATCAACACAGAAATGATAGCGCAACAAAGACTTGTGCGCTTATTTCCACCGAGTGTGGC 242357
Qy      241 TTGAGCGATAGCGCGCCCATCAAAAGGCTTTTGTGCGCGCGCTGGAAGGCAACCGT 300
Db      242356 TTGAGCGACAGCGCGCCCATCAAAAGGCTTTTGTGCGCGCGCTGGAAGGCAACCGT 242297
Qy      301 GTGCGGTGTGACGATTCAGCGGTGAGCTTCCCTGTATTCGGAAGAAATCACTGTATGCA 360
Db      242296 GTGCGGTGTGAGCATAGACGGTGTAAACCTGCTGATTTCTGAAGAAATCGCTGTAGGCC 242237
Qy      361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCGAATCGTGGCCGCAATC 420
Db      242236 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCGAATCGTGGCCGCAATC 242177
Qy      421 GAAATCGGAAGGCGCTGACTCTTCAATACCGGTAGCGCGCATTTGGTGGCGCGGTG 480
Db      242176 GAAATCGGAAGGCGCGAGACTCTTCAATACCGCGAGTGTGCTGATTTGGCGCGGTG 242117
Qy      481 AATTACCAACCTGCAAGGACATGATTTGCTGTGGACGACAGGCAATTCGGCGGTGATG 540
Db      242116 AATTACCAACCTGCAAGGCGGTGATTTGCTGTGGACGACAGGCAATTCGGCGGTGATG 242057
Qy      541 ATGAAAAACGGTTACAGCGCCCAACCGGAATGGCAAAATACACTTCGGTTTCGGGTG 600

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QY 2338 CGTAATTACCGCGTATCGTGGATTGGAAGTTTGA 2373
Db 105027 CGCAATTACCGCGTATCGTGGAAATGGAAGTTTAA 104992

RESULT 4
AAA81489_3/c
Continuation (4 of 9) of AAA81489 from base 300001 (N. meningitidis partial DNA sequence)
WP Sequence split into 9 fragments LOCUS AAA81489 Accession Aaa81489
WP Fragment Name Begin End
WP AAA81489_0 1 110000
WP AAA81489_1 100001 210000
WP AAA81489_2 200001 310000
WP AAA81489_3 300001 410000
WP AAA81489_4 400001 510000
WP AAA81489_5 500001 610000
WP AAA81489_6 600001 710000
WP AAA81489_7 700001 810000
WP AAA81489_8 800001 837096

Query Match 85.7%; Score 2038.4; DB 3; Length 110000;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 2172; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

QY 1 ATGAAACCAATTACATGCTTCTATTCGCGGCTGGTGGCAGTATTTTCGGCAATCG 60
Db 7367 ATGAAACCAATTACATGCTTCTATTCGCGGCTGGTGGCAGTATTTTCGGCAATCG 7308

QY 61 GTCTTTGGCAGCGGATGAAGTGCACACCGGTTAAAGCAGAGATAAAAGAA 120
Db 7307 GTCTTTGGCAGCAGATGAAGTGCACACCGGTTAAAGCAGAGATAAAAGCA 7248

QY 121 GTGCGGTTAAAGCCAGCTTAATCGGCTGCAACCGTGGACGTTCAACTCGGCGCG 180
Db 7247 GTGCGGTTAAAGGTCAGCGCAATGCGCTGCGGCTGGAAACGCTCAACTTAACCGT 7189

QY 181 ATTTCAACAGGAATGATAGCGACAAACAAAGACTTTGGTGGCTTACTCCACCGGCTCGCG 240
Db 7187 ATCAACAGGAATGATAGCGACAAACAAAGACTTTGGTGGCTTACTCCACCGGCTCGCG 7128

QY 241 TTGAGCGATAGCGGCGCGCATCAAAAGCTTTGTGTGCGGCGGTGGAAGGCAACCGT 300
Db 7127 TTGAGCGACAGCGGCGCGCATCAAAAGCTTTGTGTGCGGCGGTGGAAGGCAACCGT 7068

QY 301 GTGCGTGTGAGCTTGAAGCGGTGAGCTGCTGATTCGGAAGAACTCACTGTATGCA 360
Db 7067 GTGCGGCTGAGCATAGACGCTGTAACCTGCTGATTTCTGAAGAAACTCGCTGTACGCC 7008

QY 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCGAACTCGTGGCAACATC 420
Db 7007 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCGAACTCGTGGCAACATC 6948

QY 421 GAAATCGGAAAGGCGCTGACTTTTCAATACCGTAGCGCGCATTTGGTGGCGCGTG 480
Db 6947 GAAATCGTGAAGGCGCGCACTTTTCAATACCGTAGCGGTGTCATTTGGGCGCGGTG 6888

QY 481 AATTACCAACCTGCAAGGACATGATTTGCTTTGGACGACAGCAATTCGGCTGATG 540
Db 6887 AATTACCAACCTGCAAGGCGGTGATTTGCTTTGGACGACAGCAATTCGGCTGATG 6828

QY 541 ATGAAACCGTTACAGCAGCGCAACCGCAATGGACAAATACACTCGTTTCGGTGTG 600
Db 6827 ATGAAACCGTTACAGCAGCGGTAAACCGTGAATGGACAAATACACTCGTTTCGGTGTG 6768

QY 601 AGCAACGACCGGTGATCGCGCTTTGCTGATTTTCGCAACGTCGCGGTGATGAGACCGAA 660
Db 6767 AGTAACGACCGGTGATCGCGCTTTGCTGATTTTCGCAACGTCGCGGTGATGAGACCGAA 6708

QY 661 ACCGCGGCGCGGTGCTATCGGTAGAGGTGCTGGCAGCGGAGCAATTCGCTGTG 720
Db 6707 AGTGGCGGAAACCGAGGCTATGCTGTGGAAGGGGAAGGCAAGTGGCGCGGAATTCGCTGT 6648
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QY 721 TCCTCAGCGGTATCCCTGATCCGTCAAAACAATAACCAAACTTCTTGGTGAAGATT 780
Db 6647 TCGGACGCGGTATCCCTGATCCGTCAAAACAATAACCAAACTTCTTGGTGAAGATT 6588

QY 781 GCTTATCAAAATCAACGACGACCGCATCGGCCCATCGTTTAAAGCGCAGCGGGCAT 840
Db 6587 GCTTATCAAAATCAACGACGACCGCATCGGCCCATCGTTTAAAGCGCAGCGGGCAT 6528

QY 841 AATTACAGGATTGAAGAGTCTTATAACCTGACCGCTTCTTCTGCGGGAAGCCGATGAC 900
Db 6527 AATTACAGGATTGAAGAGTCTTATAACCTGACCGCTTCTTCTGCGGGAAGCCGATGAC 6468

QY 901 GTAAACAGACGCGCAATGCGCAACTCTTTTACGAATGGACGCGCTGATTTCAAAATGGCTG 960
Db 6467 GTAAACAGACGCGCAATGCGCAACTCTTTTACGAATGGATGCTGATTTCAAAATGGCTG 6408

QY 961 TCGTCTTTGAAGCGGAGCTTCGATTTACAGAACCAAAAGTGGCGGCGGTAAACACAAA 1020
Db 6407 TCGTCTTTGAAGCGGAGCTTCGATTTACAGAACCAAAAGTGGCGGCGGTAAACACAAA 6348

QY 1021 GGCTCGTTCCGACGAGTATTTCACCTGACGCGCACTATAATCAAGGATTTGGAG 1080
Db 6347 GGCTCGTTCCGACGAGTATTTCACCTGACGCGCACTATAATCAAGGATTTGGAG 6288

QY 1081 AATATATACAAACCGCAGCATGGACACCGGATTTCAACGCTTTTACTTTCCGTATGGACAGC 1140
Db 6287 GAAATATACAAACCGCAGCATGGACACCGGATTTCAACGCTTTTACTTTCCGTATGGACAGC 6228

QY 1141 CAACGCTTGCAGT---GGGCGGCAACATCGCTTGTCTTAAACTTTTCCGAGTCGG 1197
Db 6227 CATCGCTTGCAGT---GGGCGGCGGCGACACCGCTGTCTTAAACTTTTCCGAGTCGG 6168

QY 1198 CGTGAAGTTTGAAGAACTTAAACCGCGACGATTAATTTTACGCGAAAGATATCCCGTACT 1257
Db 6167 CGTGAAGTTTGAAGAACTTAAACCGCGACGATTAATTTTACGCGCGCGTGTGTTCGAACC 6108

QY 1258 ACCAGCTGATTTCAACACCCCGTGAAGAAACCACTAATTAATGTTTCTCACTGCTGATCAA 1317
Db 6107 ACCAGCAGTATCCAGCATCCCGTGAAGAAACCACTAATGTTTCTCACTGCTGATCAA 6048

QY 1318 ATCCAAATGGAACGAGTGTTCAGCAGCGCTGCAGATATCCCGTTAGCATATACCAAAATG 1377
Db 6047 ATTCAATGGAACGAGTGTTCAGTAGCGCGCAGGATTCGCTTACGACCAACCAAAATG 5988

QY 1378 AGCCTCAGGAATTTGAATGCGAGTGTCTATGTCAGAAAAACACCCCTGCGACCCAAAT 1437
Db 5987 AGCCTCAGGAATTTGAATGCGAGTGTCTATGTCAGAAAAACACCACTGCGACCCAAAT 5928

QY 1438 ACTTATAAGGCTGGAGCGGATTTGTCGGTTTGGCGCGCAACTGAATCAGGCTTTGGCAT 1497
Db 5927 ACTTATAAGGCTGGAGCGGATTTGTCGGTTTGGCGCGCAACTGAATCAGGCTTTGGCAT 5868

QY 1498 GTCGGTTACGACATTAATTCGGCTACCGTGTCCCAATGCGTCCGAAGTGTATTTCACT 1557
Db 5867 GTCGGTTACGACATTAATTCGGCTACCGTGTCCCAATGCGTCCGAAGTGTATTTCACT 5808

QY 1558 TACAACACCGTTCGGGTAAATTTGGCTGCCCAATCCCAACCTGAAAGCGGAGCGAGCACC 1617
Db 5807 TACAACACCGTTCGGGTAAATTTGGCTGCCCAATCCCAACCTGAAAGCGGAGCGAGCACC 5748

QY 1618 ACCCAACCTCTCTGCAAGGCGCGACGAAAAAGGTACTTTGGATGCCAACCTGTAT 1677
Db 5747 ACCCAACCTCTCTGCAAGGCGCGACGAAAAAGGTACTGTGATGCCAACCTGTAT 5688

QY 1678 CAAAACAAATACCGCAACTTCTTCTGAAGAGCAGAGCTGACCAACGAGCGGCGATGTC 1737
Db 5687 CAAAACAAATACCGCAACTTCTTCTGAAGAGCAGAGCTGACCAACGAGCGGCGATGTC 5628

QY 1738 GGCTGTACTCAGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1797
Db 5627 GGCTGTACTCAGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5568

QY 1798 GAATGGCAGATGCAAAATATCGATAAGGCCCGCAATCCCGTGTCTTTGAGCTGACAGCGCGT 1857
```







Db 1921 TATCGAAGAAAGCAAACTGTCGGGCGACACAGCGCTGCTCCACACAGCCGCGGAAAGTG 1980  
Qy 1981 ATTCCCGGTGTCGACTACGAAAGCCGAGCGAAATAGGGGTGTGTTCTCCGCGTGAAT 2040  
Db 1981 ATTCCCGGTGTCGACTACGAAAGCCGAGCGAAATAGGGGTGTGTTCTCCGCGTGAAT 2040  
Qy 2041 TATCTGGTGCAGAAAGGCCAAGAGCGCGCAATACACACCGTTTATGAAACCAAGGGCCGG 2100  
Db 2041 TATCTGGTGCAGAAAGGCCAAGAGCGCGCAATACACACCGTTTATGAAACCAAGGGCCGG 2100  
Qy 2101 GGTAACGCTTTGCGAGAAAGGTAAAGATTTACCGGTGCTGACCAAGTGGCTTATGTG 2160  
Db 2101 GGTAACGCTTTGCGAGAAAGGTAAAGATTTACCGGTGCTGACCAAGTGGCTTATGTG 2160  
Qy 2161 TTTGATATGACGGCTTCTACAACTGGCTTAAACCTGACTTTCGTCGAGGCGTATAT 2220  
Db 2161 TTTGATATGACGGCTTCTACAACTGGCTTAAACCTGACTTTCGTCGAGGCGTATAT 2220  
Qy 2221 AATGTGTTCAACCGCAATACACCACTTGGGATTCCTCGCGGTTTGTATAGCTACAGC 2280  
Db 2221 AATGTGTTCAACCGCAATACACCACTTGGGATTCCTCGCGGTTTGTATAGCTACAGC 2280  
Qy 2281 ACCACCAACCGGTCGACCGAGATGCGAAAGGCTTAGACCGCTACCGCGCTCAGGCGGT 2340  
Db 2281 ACCACCAACCGGTCGACCGAGATGCGAAAGGCTTAGACCGCTACCGCGCTCAGGCGGT 2340  
Qy 2341 AATTACCGCTATCGCTGGATTCGAAAGTTTGAATTC 2378  
Db 2341 AATTACCGCTATCGCTGGATTCGAAAGTTTGAATTC 2378

RESULT 2  
AAA81460  
ID AAA81460 standard; DNA; 20844 BP.  
XX AC  
XX AAA81460;  
XX  
XX 04-DEC-2000 (first entry)  
DE N. meningitidis partial DNA sequence gnm\_8 SEQ ID NO:8.  
XX  
XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;  
KW Meningococcus B; MenB; ds.  
XX  
XX Neisseria meningitidis.  
XX OS  
XX WO200022430-A2.  
XX  
XX 20-APR-2000.  
XX  
XX 08-OCT-1999; 99WO-US023573.  
XX  
XX 09-OCT-1998; 98US-0103794P.  
XX 30-APR-1999; 99US-0132068P.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
PI Rappuoli R, Pizza M;  
XX  
XX WPI; 2000-318079/27.  
XX  
XX Isolated nucleotide sequences of Neisseria meningitidis which can be used  
PT in the diagnosis and treatment of N. meningitidis infection and other  
PT Neisserial infections, for example, N.gonorrhoea.  
XX  
XX Claim 7; Page 320-326; 1760pp; English.  
PS  
XX The present invention describes methods of obtaining immunogenic proteins  
XX from Neisseria genomic sequences. AAA81453 to AAA82414 represent  
CC

CC specifically claimed Neisseria meningitidis genomic DNA sequences;  
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA  
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and  
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of  
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent  
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all  
CC used in the exemplification of the present invention. The nucleic acid  
CC sequences, protein sequences, and antibodies against them, can be used in  
CC the manufacture of a composition. The composition can be used as a  
CC medicament (or in the manufacture of a medicament) for treating,  
CC preventing or diagnosing infection due to Neisserial bacteria. For  
CC example, some of the identified proteins could be components of vaccines  
CC against Meningococcus B; against all serotypes; and/or against all  
CC pathogenic Neisseriae. Identification of sequences from the bacterium  
CC will also facilitate production of biological probes, particularly  
CC organism-specific probes. Attempts to make efficacious Meningococcus B  
CC vaccines have failed mainly due to antigen tolerance. Multivalent  
CC vaccines have also been tried but none have successfully overcome  
CC antigenic variability. The provision of further, complete sequences may  
CC provide an opportunity to identify secreted or surface exposed proteins  
CC that may be presumed targets for the immune system and which are not  
CC antigenically variable or at least more conserved than other more  
CC variable regions  
XX  
SQ Sequence 20844 BP; 5244 A; 5005 C; 5645 G; 4949 T; 0 U; 1 Other;  
Query Match 85.7%; Score 2038.4; DB 3; Length 20844;  
Best Local Similarity 91.4%; Pred. No. 0;  
Matches 2172; Conservative 0; Mismatches 201; Indels 3; Gaps 1;  
Qy 1 ATGAAACCAATTACACATGCTTCTTATGCGCGCTGTCGGCAGTATTTTCGGCAATCCG 60  
Db 6854 ATGAAACCAATTACAAATGCTCCTATCGCGCGCTGTCGGCAGTATTTTCGGCAATCCG 6913  
Qy 61 GTCTTGGCAGCGGATGAAGCTGCAACGAAACACACACCGCTTAAAGCAGAGATAAGAA 120  
Db 6914 GTCTTGGCAGCAGATGAAGCTGCAACTGAACACACACCGCTTAAAGCAGAGATAAGAA 6973  
Qy 121 GTGCGGTTAAAGACACAGCTTAATGCGCTGCAACCGTGAACGCTGTCAACCTCGGCGC 180  
Db 6974 GTGCGGTTAAAGGTGAGCGCAATGCGCTGCGCTGTGGAACGCTCAACCTTAACCGT 7033  
Qy 181 ATTCAACAGGAAATGATACGCGCAACAAAGACTTGTGCGTTACTTCCACCGAGTCGCG 240  
Db 7034 ATCAACAAAGAAATGATACGCGCAATAAAGACTTGTGCGCTTATTCACCGAGTGTGCG 7093  
Qy 241 TTGAGCGATAGCGCGCCCATCAAAAGGCTTGTGTCGCGCGCTGGAAGCGCAACCGT 300  
Db 7094 TTGAGCGACAGCGCGCCCATCAAAAGGCTTGTGTCGCGCGCTGGAAGCGCAACCGT 7153  
Qy 301 GTGCGGTGTCAGCAATTGACGCGGTGAGCTTCCTGATTTCGGAAGAAACTCACTGTATGCA 360  
Db 7154 GTGCGGTGAGCAATGACGCGGTGTAACCTGCTGATTTCGAAGAAACTGCTGTATGCC 7213  
Qy 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATGACCCCGAATCTGTGCGCAACATC 420  
Db 7214 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATGACCCCGAATCTGTGCGCAACATC 7273  
Qy 421 GAAATCGGAGGCGGCTGACTTTTCATACCGGTAGCGCGCTGAGGCGCGGTG 480  
Db 7274 GAAATCGTGAAGGCGGCGAGCTCTTTCAATACCGGAGTGTGTCATTTGGCGCGGTGTG 7333  
Qy 481 AATTACCAACCTGCAAGGACATGATTTGCTGTGGACGACAGGCAATTCGCGGTGATG 540  
Db 7334 AATTACCAACCTGCAAGGCGGTGATTTGCTGTGGACGACAGGCAATTCGCGGTGATG 7393  
Qy 541 ATGAAACCGGTTACGAGCGCGCAACCGGCAATGGAACAATACATCTCGGTTTCGGTGTG 600  
Db 7394 ATGAAACCGGTTACGAGCGCGTAACCGGTAATGGAACAATACATCTCTCGGTTTCGGTGTG 7453  
Qy 601 AGCAACGACCGCGTGGATGCGCTTTCGCTGATTTCGCAACGCTCGCGTCAATGACCGAA 660  
Db 7454 AGTAACGACCGCGTGGATGCTGCTGCTGATTTCGCAACGCTCGCGTCAATGAAACCGAA 7513



CC (Hmbr) (AAR95567) of *N. gonorrhoeae* strain MS11A. It was obtd. by PCR  
 CC amplification of genomic DNA using primers (AAT27001-02) based on the *N.*  
 CC meningitidis serotype C hmrB gene (see also AAT26997). The gene can be  
 CC used to prepare recombinant haemoglobin receptor protein, useful as a  
 CC vaccine for gonorrhea. It can be expressed in attenuated *Salmonella* host  
 CC cells. It can also be utilised as a probe to detect infection in humans.  
 CC hmrB genes for *N. meningitidis* serotype A (AAT26998) and B (AAT26999)  
 CC were similarly obtd. (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX

SQ Sequence 2378 BP; 629 A; 618 C; 606 G; 525 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 2378; DB 2; Length 2378;  
 Best Local Similarity 100.0%; Pred. NO. 0;  
 Matches 2378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAACCAATTACATGCTTCTTATTTGCGCGCTGGTGGCAGTATTTTCGGCAATCCG 60  
 DB 1 ATGAACCAATTACATGCTTCTTATTTGCGCGCTGGTGGCAGTATTTTCGGCAATCCG 60  
 QY 61 GTCTTGGCAGCGATGAAGCTGCAACCGAACCACACCCGTTTAAAGCAGAGATAAAGAA 120  
 DB 61 GTCTTGGCAGCGATGAAGCTGCAACCGAACCACACCCGTTTAAAGCAGAGATAAAGAA 120  
 QY 121 GTGCGGTTTAAAGACCAAGCTTAAATGCGCTGCAACCGTGGAACTGTCACCTCGGCGC 180  
 DB 121 GTGCGGTTTAAAGACCAAGCTTAAATGCGCTGCAACCGTGGAACTGTCACCTCGGCGC 180  
 QY 181 ATTCAACAGGAATGATACGCGAACAACAAAGACTTGGTGGTATCTCCACCGACGTGCGC 240  
 DB 181 ATTCAACAGGAATGATACGCGAACAACAAAGACTTGGTGGTATCTCCACCGACGTGCGC 240  
 QY 241 TTGAGCGATAGCGCGCCCATCAAAAGGCTTGTGTCGGCGGCTGGAAGCAACCGT 300  
 DB 241 TTGAGCGATAGCGCGCCCATCAAAAGGCTTGTGTCGGCGGCTGGAAGCAACCGT 300  
 QY 301 GTCGGTGTGAGCAATTCACGCGTGAGCTGCTGCTGATTTCGGAAGAAACTCACTGTATGCA 360  
 DB 301 GTCGGTGTGAGCAATTCACGCGTGAGCTGCTGCTGATTTCGGAAGAAACTCACTGTATGCA 360  
 QY 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCGAACTCGTGGCGCAACATC 420  
 DB 361 CGTTATGGCAACTTCAACAGCTCGCGCTGTCTATCGACCCCGAACTCGTGGCGCAACATC 420  
 QY 421 GAAATCGGAAGGCGCTGACTTTCAATACCGGTAGCGGCGCATTTGGTGGCGCGCTG 480  
 DB 421 GAAATCGGAAGGCGCTGACTTTCAATACCGGTAGCGGCGCATTTGGTGGCGCGCTG 480  
 QY 481 AATTACCAAAACCTGCAAGGACATGATTTGCTGTCGACGACAGGCAATTCGGCGTGTATG 540  
 DB 481 AATTACCAAAACCTGCAAGGACATGATTTGCTGTCGACGACAGGCAATTCGGCGTGTATG 540  
 QY 541 ATGAAAAACGGTTACAGCAGCGCAACCGGAATGGAACAATACTACCTCGTTTCGGTGTG 600  
 DB 541 ATGAAAAACGGTTACAGCAGCGCAACCGGAATGGAACAATACTACCTCGTTTCGGTGTG 600  
 QY 601 AGCAACGACGCGTGTGATCGCGTTTCTGTTATTCGCAACGTCGCGTTCATGAGCCGAA 660  
 DB 601 AGCAACGACGCGTGTGATCGCGTTTCTGTTATTCGCAACGTCGCGTTCATGAGCCGAA 660  
 QY 661 AGCGCGGCGAGCGTGGCTATCCGCTAGAGGGTGTGGCAGCGGAGCAATTAATCCGTTGT 720  
 DB 661 AGCGCGGCGAGCGTGGCTATCCGCTAGAGGGTGTGGCAGCGGAGCAATTAATCCGTTGT 720  
 QY 721 TCGTCAACGGGTATCCCTGATCCGTCGCAACCAAAATACCAAACTTCTTGGGTAAAGATT 780  
 DB 721 TCGTCAACGGGTATCCCTGATCCGTCGCAACCAAAATACCAAACTTCTTGGGTAAAGATT 780  
 QY 781 GCTTATCAATCAACGACAGCAACCGCATCGGCCCATCGTTTAAACCGGCAGCGGGGCAT 840  
 DB 781 GCTTATCAATCAACGACAGCAACCGCATCGGCCCATCGTTTAAACCGGCAGCGGGGCAT 840

QY 841 AATTACAGATTTGAAGAGTCTTTATAAAGCTGACCGCTCTTCTCTGCGGGAAGCCGATGAC 900  
 DB 841 AATTACAGATTTGAAGAGTCTTTAACTCTGACCGCTTCTTCTGCGGGAAGCCGATGAC 900  
 QY 901 GTAAACAGACGCGCAATGCGCAACCTCTTTTACGAATGAGCGCCTGATTTCAAATTTGGCTG 960  
 DB 901 GTAAACAGACGCGCAATGCGCAACCTCTTTTACGAATGAGCGCCTGATTTCAAATTTGGCTG 960  
 QY 961 TCGTCTTTGAGAGGCGGACTTCGATTTATCAGAACCAAGTGGCGCGGTAAACACAA 1020  
 DB 961 TCGTCTTTGAGAGGCGGACTTCGATTTATCAGAACCAAGTGGCGCGGTAAACACAA 1020  
 QY 1021 GGCTCTTTCCGACCGGATTTATTCACCTGGAGCGCAACTATAATCAGAAGATTGGAG 1080  
 DB 1021 GGCTCTTTCCGACCGGATTTATTCACCTGGAGCGCAACTATAATCAGAAGATTGGAG 1080  
 QY 1081 AATAATACACCGCAGCATGGAACAACCGATTTCAAACGTTTTTACTTTGGGTATGACACG 1140  
 DB 1081 AATAATACACCGCAGCATGGAACAACCGATTTCAAACGTTTTTACTTTGGGTATGACACG 1140  
 QY 1141 CAACCGTTGCAACTGGCGGCGCAACATCGCTTGTGCTTAAACCTTTGCCAGTGGCGT 1200  
 DB 1141 CAACCGTTGCAACTGGCGGCGCAACATCGCTTGTGCTTAAACCTTTGCCAGTGGCGT 1200  
 QY 1201 GAGTTTGAACCTTAAACCGCGCAGATTTATTAATTCAGCGAAAGAGTATCCCGTACTAC 1260  
 DB 1201 GAGTTTGAACCTTAAACCGCGCAGATTTATTAATTCAGCGAAAGAGTATCCCGTACTAC 1260  
 QY 1261 AGCTCGATTTCAACACCCCGTGAACCACTAATTAATTTGTTTCTCACTGCTCTGATCAATC 1320  
 DB 1261 AGCTCGATTTCAACACCCCGTGAACCACTAATTAATTTGTTTCTCACTGCTCTGATCAATC 1320  
 QY 1321 CAATGGAACGAGCTGTTGAGCAGCGCTGAGATATCCGTTACGATCATACCAAAATGACG 1380  
 DB 1321 CAATGGAACGAGCTGTTGAGCAGCGCTGAGATATCCGTTACGATCATACCAAAATGACG 1380  
 QY 1381 CCTCAGGAATTTGAATTCGCGAGTGTATGTTGACAAACACCCGCTGACGCAATATCT 1440  
 DB 1381 CCTCAGGAATTTGAATTCGCGAGTGTATGTTGACAAACACCCGCTGACGCAATATCT 1440  
 QY 1441 TATAAAGGCTGAGCGGATTTGTCGGTTTGGCGGCGCAACTGAATCAGGCTTTGGCATGTC 1500  
 DB 1441 TATAAAGGCTGAGCGGATTTGTCGGTTTGGCGGCGCAACTGAATCAGGCTTTGGCATGTC 1500  
 QY 1501 GGTACGACATTTACTTTCGGCTACCGTGTCCCAATGCGTCCGAAAGTGTATTTCACTTAC 1560  
 DB 1501 GGTACGACATTTACTTTCGGCTACCGTGTCCCAATGCGTCCGAAAGTGTATTTCACTTAC 1560  
 QY 1561 AACACCGGTTTGGGTAAATTTGGCTGCCCAATCCAACTGAAAGCGGAGCGGACCAAC 1620  
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 DB 1741 TGTACTCAGATGAATTTACTACTTACTACGATGTTAGCAATCTTATTTCCGAAAAACCGGAA 1800  
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 QY 1921 TATGCGAAAAAGCAAACTGTGCGGCGCAACACGCTGCTGTCCACACAGCGCGGAAAGTG 1980

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 14:52:34 ; Search time 1270 Seconds  
(without alignments)  
11084.366 Million cell updates/sec

Title: US-09-665-358-7  
Perfect score: 2378  
Sequence: 1 ATGAACCAATACACATGCT.....GATTGGAAGTTTGAATTC 2378

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*  
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2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	2038.4	85.7	110000	3	AA81489 2
4	2038.4	85.7	110000	3	AA81489 3
5	2038.4	85.7	34980	3	AA81489 4
6	1988.6	83.6	2379	2	AAT26999
7	1979.2	83.2	2373	2	AAT26997
8	1846.4	77.6	2376	2	AAT26998
9	840.8	35.4	852	10	ABZ37973
10	833.8	35.1	864	10	ABZ37953
11	344.8	14.5	348	10	ABZ37945
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14	103.4	4.3	2427	10	ABZ38258
15	78.6	3.3	2880	4	AAD05317
16	78.2	3.3	2751	4	AAD05364
17	74	3.1	3300	6	ABZ67377
18	72	3.0	14652	3	AA81482
19	72	3.0	110000	3	AA81489_1
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22	68.4	2.9	1767	11	ABD15812	Abd15812 Pseudomon
23	68.4	2.9	3738	11	ABD15760	Abd15760 Pseudomon
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25	66.6	2.8	2736	10	ABZ41276	Abz41276 N. gonorr
26	65.4	2.8	2809	2	AAQ55618	AAQ55618 N.meningi
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28	65	2.7	3286	2	AAQ78929	AAQ78929 N.gonorrh
29	65	2.7	3286	6	AAD32061	Aad32061 Neisseria
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33	64.2	2.7	34980	3	AAF21607	AAF21607 Neisseria
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35	63.6	2.7	2370	11	ABD11836	Abd11836 Pseudomon
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37	61.4	2.6	2000	8	ADA71938	Ada71938 Rice gene
38	60.8	2.6	2826	2	AAT38071	Aat38071 Transferr
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40	60.6	2.5	49617	4	AAF28541	AAF28541 Genomic f
C 41	60.4	2.5	110000	2	AAT42063_06	Continuation (7 of
42	59	2.5	3144	13	ADT05700	Adt05700 Haemophil
C 43	59	2.5	106645	13	ADT05645	Adt05645 Haemophil
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C 45	58.6	2.5	5562	13	ADT05480	Adt05480 Haemophil

## ALIGNMENTS

RESULT 1  
AAT27000  
ID AAT27000 standard; cDNA; 2378 BP.

XX AC AAT27000;  
XX DT 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 28-AUG-1996 (first entry)  
XX DE N. gonorrhoeae haemoglobin receptor cDNA.

XX Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; gonorrhoea;  
KW ss.

OS Neisseria gonorrhoeae.

XX Key Location/Qualifiers

FT CDS 1..2373  
FT /\*tag= a

XX WO9612020-A2.

XX PD 25-APR-1996.

XX PF 17-OCT-1995; 95WO-US013623.

XX PR 18-OCT-1994; 94US-00326670.

XX PR 02-OCT-1995; 95US-00537361.

XX PA (UYOR-) UNIV OREGON HEALTH SCI.

XX PI Stojiljkovic I, So M, Hwa V, Heffron F, Nassif X;

XX DR WPI; 1996-222006/22.

XX DR P-PSDB; AAR95568.

XX PT DNA encoding Neisseria haemoglobin receptor proteins - for use in  
PT preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.  
XX Claim 5; Page 64-66; 104pp; English.

XX CC A DNA sequence (AAT27000) codes for the bacterial haemoglobin receptor

541 ATGAAAAACGGTTACAGACGCGCAACCGCGAATGGAACAAATACACTCGGTTTCGGTGTG 600  
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 601 AGCAACGACCGCGGTGAGATGCGCTTGTGTATTCGCAACGTCGGCGTCAAGAGACCGAA 660  
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 781 GCTTATCAAAATCAACGACCAACGCGATCGGCCCATCGTTTAAACGCGCAGCGGGCAT 840  
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 841 AATTACAGATTGAAGAGTCTTATACCTGACCGCTCTCTCTGGCGGAGCGCATGAC 900  
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## RESULT 10

AF133695  
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 DEFINITION  
 Neisseria meningitidis Hemo (hmr) gene, complete cds.  
 ACCESSION  
 AF133695  
 VERSION  
 AF133695.1  
 KEYWORDS  
 GI:6692577  
 ORGANISM  
 Neisseria meningitidis  
 Neisseria meningitidis  
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 Neisseriaceae; Neisseria.  
 REFERENCE  
 1 (bases 1 to 1500)  
 Zhu, W., Hunt, D.J., Richardson, A.R. and Stojiljkovic, I.  
 Use of heme compounds as iron sources by pathogenic neisseriae  
 requires the product of the hmr gene  
 J. Bacteriol. 182 (2), 439-447 (2000)  
 MEDLINE  
 20096688  
 PUBMED  
 10629191  
 REFERENCE  
 2 (bases 1 to 1500)  
 Hunt, D.J., Richardson, A.R. and Stojiljkovic, I.

Qy	1555	ACTTACACCAAGCGTTCGGGTAATGCTGCCCAATCCCAACCTCCGAAGCGGCGAGC	1614
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Db	1905	GTCCGCTGTAATCAGATGAATTAATCTACCGTATGTAAGCAATCTTATTCGAAAAA	1964
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Db	1965	CTGGAATGGCAGATGCAAAATATGATAAGCCCGAATCCGTTGCTTTGAGCTGACAGC	2024
Qy	1855	CGTCTGAATGTGCAAAAGTAGCGTCTTTGTTCTGAGGGCTGGAATTTGTTCCGCTCG	1914
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RESULT 9  
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LOCUS NMU40860 2568 bp DNA linear BCT 13-NOV-1996  
DEFINITION Neisseria meningitidis hemoglobin receptor (hmbR) gene, complete cds.  
ACCESSION U40860  
VERSION U40860.1 GI:1666680  
KEYWORDS  
SOURCE Neisseria meningitidis  
ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
1 (bases 1 to 2568)  
Stojiljkovic, I., Larson, J., Hwa, V., Anic, S. and So, M.  
AUTHORS Stojiljkovic, I., Larson, J., Hwa, V., Anic, S. and So, M.  
TITLE Direct Submission  
JOURNAL Submitted (19-NOV-1995) Igor Stojiljkovic, Microbiology &

FEATURES	Immunology, OHSU, L220, Portland, OR 97201, USA
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ORIGIN

Query Match	77.6%;	Score 1844.4;	DB 1;	Length 2568;
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Db	143	GTCTTTGCGGAGATGAGCTGCAACTGAAACACACACCCGTTTAAAGCAGAGATAAAGCA	202	
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1323..1331
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tract, controls phase variable expression; the 'on'
configuration contains 9 G residues, the 'off'
configuration contains 10 G residues"

ORIGIN
Query Match      83.5%; Score 1985.4; DB 1; Length 2652;
Best Local Similarity 90.2%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches 226; Indels 6; Gaps 2;

QY      1 ATGAAACCAATTACATGCTTCTATTGCGCGCTGGTGGCGAGTATTTTGGCAATCCG 60
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QY      61 GTCTTGGCAGCGATGAAGCTCAACCCGAAACACACCCGTTTAAAGCAGAGATAAGAA 120
DB      225 GTCTTGGCAGCGATGAAGCTCAACCTGAACCAACACCCGTTTAAAGCAGAGATAAGAA 284
QY      121 GTGCGGCTTAAAGACGAGCTTAATGCGCTGCAACCGTGGAAACGTGTCAACCTCGGCCG 180
DB      285 GTACGGCTTAAAGCGCAGCGATGCGCTGCGGCTGTGGAACGCGTCAACCTTAACCGT 344
QY      181 ATTCAACAGGAATGATACGCAACAAAGACTTGGTGGTGTACTTCCACCGACGTCGCG 240
DB      345 ATCAAAACAGGAATGATACGCAACAAAGACTTGGTGGTGTACTTCCACCGACGTCGCG 404
QY      241 TTGAGCGATAGCGCGCCATCAAAAGCTTTGCTGTGCGCGGCTGGAAGCAACCGT 300
DB      405 TTGAGCGATAGCGCGCCATCAAAAGCTTTGCTGTGCGCGGCTGGAAGCAACCGT 464
QY      301 GTGCGGTGTGAGCATTTGACGCGGTGAGCTGCTGCTGATTCGGAAGAAACTCACTGTATGCA 360
DB      465 GTGCGGTGTGAGCATAGACGCGGTAAACCTGCTGATTCGGAAGAAACTCACTGTATGCG 524
QY      361 CTTATGCAACTTCAACAGCTGCGCCTGTCTATGACCCCGAACTCGTGGCGCAACATC 420
DB      525 CGTTATGCAACTTCAACAGCTGCGCCTGTCTATGACCCCGAACTCGTGGCGCAACATC 584
QY      421 GAAATGCGCAAGGGCGCTCACTCTTTCATACGCTAGCGGCGCATTTGGTGGCGCGGTG 480
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RESULT 8  
AF105339  
LOCUS  
DEFINITION  
Neisseria meningitidis hemoglobin receptor (hmbR) gene, complete cds.  
ACCESSION  
AF105339  
VERSION  
AF105339.1  
KEYWORDS  
GI:6606086  
SOURCE  
Neisseria meningitidis  
ORGANISM  
Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
REFERENCE  
1 (bases 1 to 2652)  
AUTHORS  
Lewis, L.A., Gibson, M., Hartman, K., Ownbey, T., Vaughn, J., and Dyer, D.W.  
TITLE  
Phase variation of HpuAB and HmbR, two distinct haemoglobin receptors of *Neisseria meningitidis* DNM2  
JOURNAL  
Mol. Microbiol. 32 (5), 977-989 (1999)  
MEDLINE  
99291064  
PubMed  
10361300  
REFERENCE  
2 (bases 1 to 2652)  
AUTHORS  
Lewis, L.A., Gibson, M., Hartman, K., Vaughn, J., and Dyer, D.W.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (10-NOV-1998) Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 S.L. Young Blvd., Oklahoma City, OK 73104, USA  
FEATURES  
Location/Qualifiers



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## RESULT 7

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LOCUS NM040859 2632 bp DNA linear BCT 13-NOV-1996
DEFINITION Neisseria meningitidis hemoglobin receptor (hmbR) gene, complete
cds.
ACCESSION U40859
VERSION U40859.1 GI:1666678
KEYWORDS
SOURCE
ORGANISM Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2632)
AUTHORS Stojiljkovic, I., Larson, J., Hwa, V., Anic, S. and So, M.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-1995) Igor Stojiljkovic, Microbiology &
Immunology, OHSU, L220, Portland, OR 97201, USA
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## ORIGIN

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Query Match 83.6%; Score 1987.2; DB 1; Length 2632;
Best Local Similarity 90.1%; Pred. No. 0;
Matches 2140; Conservative 0; Mismatches 233; Indels 3; Gaps 1;
Qy 1 ATGAACCATTTACATGCTTCTTATTCGCGCGCTGTCGCGAGTATTTTCGCGCAATCCG 60
Db 174 ATGAACCATTTACATGCTTCTTATTCGCGCGCTGTCGCGAGTATTTTCGCGCAATCCG 233
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Db 234 GTCTTGGCAGCAGATGAAGCTGCAACCGAAACACACCCGTTTAAAGCAGAGATAAAGCA 293
Qy 121 GTGCGCGTTAAAGACAGCTTAATCGCGCTGCAACCGTGGAAACGTTGCAACCTCGCGCGC 180
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Db 714 ATGAAAACCGTTTACAGCAGCGGTAAACCGTGAATGGAACAAATACCTTCGTTTCGCTGTG 773
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Db 2810 AGCGTAATACGCGGTATCGCTGGATGGAAATTTTAA 2848

## RESULT 6

LOCUS I85729 3318 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 1 from patent US 5698438.  
ACCESSION I85729  
VERSION I85729.1 GI:3205447

## KEYWORDS

Unknown.

## SOURCE

Unknown.

## ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 3318)

AUTHORS Scojliljkovic, I., So, M., Hwa, V., Heffron, P. and Nassif, X.

TITLE Bacterial hemoglobin receptor gene

JOURNAL Patent: US 5698438-A 1 16-DEC-1997;

FEATURES Location/Qualifiers

source 1..3318

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## ORIGIN

Query Match 83.6%; Score 1988.6; DB 6; Length 3318;  
Best Local Similarity 90.3%; Pred No. 0;  
Matches 2149; Conservative 0; Mismatches 224; Indels 6; Gaps 2;  
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Db 470 ATGAACCAATTACAAATGCTCCCTATCGCGGCTGTCGCGAGTATTTTCGGAATCCG 529  
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VERSION U18558.1 GI:687639  
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ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
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REFERENCE 1 (bases 1 to 3318)  
AUTHORS Stojiljkovic, I., Hwa, V., de Saint Martin, L., O'Gaora, P., Nassif, X., Heffron, F. and So, W.  
TITLE The Neisseria meningitidis haemoglobin receptor: its role in iron utilization and virulence  
MOL. MICROBIOL. 15 (3), 531-541 (1995)  
MEDLINE 95302964  
PUBMED 7783623  
REFERENCE 2 (bases 1 to 3318)  
AUTHORS Stojiljkovic, I.  
DIRECT SUBMISSION  
TITLE Submitted (13-DBC-1994) Igor Stojiljkovic, Microbiology and Immunology, Oregon Health Sciences University, Portland, OR 97201, USA  
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VERSION        AL162757.2
KEYWORDS       GI:7380371
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ORGANISM       Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS        Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C.,
Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T.,
Davies, R.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N.,
Holroyd, S., Jagers, K., Leather, S., Moule, S., Mungall, K.,
Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M.,
Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G.
TITLE          Complete DNA sequence of a serogroup A strain of Neisseria
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JOURNAL        Nature 404 (6777), 502-506 (2000)
MEDLINE        20222556
PubMed        10761919
REFERENCE      2 (bases 1 to 326301)
AUTHORS        Parkhill, J.
TITLE          Direct Submission
JOURNAL        Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT
Notes:
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
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fasta scores; E(): 0, 96.7% identity in 183 aa overlap.
Contains Pfam match to entry PF00127 copper-bind, Copper
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Qy 121 GTGCGCGTTAAAGACCAAGTAAATCGGCTGCACACCGTGGAAACGTTCAACCTCGCGCG 180

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Db 7389 TCGTCACCGGTATCCCTGATCCGTCGCAAAACAAATACCAAACTCTTCTGGTGAAGTT 7330

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Qy 841 AATTACAGATGAAGAGTCTTATTAACCTGACCGCTTCTTCTGGCGGGAACCGCATGAC 900

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ACCESSION AE002517 AE002098
VERSION   AE002517.1 GI:7226912
SOURCE   Neisseria meningitidis MC58
ORGANISM Neisseria meningitidis MC58
REFERENCE 1 (bases 1 to 14228)
AUTHORS Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C.,
Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F.,
Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D.,
Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D.,
Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blair,E.,
Cittoni,H., Clark,E.B., Cotton,M.D., Utterback,T.R., Khouri,H.,
Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Massignani,V.,
Piazza,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R.,
Rappuoli,R. and Venter,J.C.
Complete genome sequence of Neisseria meningitidis serogroup B
strain MC58
JOURNAL Science 287 (5459), 1809-1815 (2000)
MEDLINE 20175755
PUBMED 10710307
REFERENCE 2 (bases 1 to 14228)
AUTHORS Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C.,
Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F.,
Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D.,
Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D.,
Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blair,E.,
Cittoni,H., Clark,E.B., Cotton,M.D., Utterback,T.R., Khouri,H.,
Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Massignani,V.,
Piazza,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R.,
Rappuoli,R. and Venter,J.C.
Direct Submission
TITLE Submitted (17-MAR-2000) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr, Rockville, MD 20850, USA
FEATURES
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GRSLATIPKVRDMAREAGNDVAVTNGQFALLHGKTVREVPMDAGLMGRVCAHLDGL
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KLDVLEQIKAEHNRKKPFLTVNTLPHNSKLTFFVADMEPLIAMKDALIMADPGLI
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ELEVFHIGALCIAYSGRLCSGFNHRDPQGGCTNSCRWDYKHNATEDAGDAQLL
QGFNFEKAQEKNQNFEGINGQRHPYADKFLIEESNRPEGMFIMEDSHGTYIMNS
KDLRGIEVVEKLAKIGVDSLKVEGRTKSLYVARVAQSYRAIKDADDAVGRPFYDLSL

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Query Match		98.1%;	Score 2331.8;	DB 1;	Length 2605;		
Best Local Similarity		99.0%;	Pred. No. 0;				
Matches 2356;		Conservative	0;	Mismatches	22;	Indels	1; Gaps 1;
QY	1	ATGAACCAATTAACATGCTTCTTATTCGCGCGTGGTCCGAGTATTTTCGGCAATCCG	60				
DB	164	ATGAACCAATTAACATGCTTCTTATTCGCGCGTGGTCCGAGTATTTTCGGCAATCCG	223				
QY	61	GTCTTGGCAGCGATGAAGCTCCACCGCAACACACCCGTTTAAAGCAGAGATAAGAA	120				
DB	224	GTCTTGGCAGCGATGAAGCTCCACCGCAACACACCCGTTTAAAGCAGAGATAAGAA	283				
QY	121	GTGCGGTTTAAAGACAGCTTAAATGCGCTCGCAACCGTGGAAAGCTGTCAACCTCGCGCGC	180				
DB	284	GTGCGGTTTAAAGACAGCTTAAATGCGCTCGCAACCGTGGAAAGCTGTCAACCTCGCGCGC	343				
QY	181	ATTCAACAGGAATGATACGCGACAAACAAAGACTTGGTGGCTTACTCCACCGAGCTGGCG	240				
DB	344	ATTCAACAGGAATGATACGCGACAAACAAAGACTTGGTGGCTTACTCCACCGAGCTGGCG	403				
QY	241	TTGAGCGATAGCGCGCCCATCAAAAGGCTTTGCTGTGCGCGGCTGGAAGGCAACCGT	300				
DB	404	TTGAGCGATAGCGCGCCCATCAAAAGGCTTTGCTGTGCGCGGCTGGAAGGCAACCGT	463				
QY	301	GTGCGGTGTGAGCAATGACCGCGTGAGCCTGCCTGATTCGGAAGAAACTCACTGTATGCA	360				
DB	464	GTGCGGTGTGAGCAATGACCGCGTGAGCCTGCCTGATTCGGAAGAAACTCACTGTATGCA	523				
QY	361	CGTTATGGCAATTCACAGCTCGCGCTGTCTATCGACCCGAACTCGTGGCGCAACATC	420				
DB	524	CGTTATGGCAATTCACAGCTCGCGCTGTCTATCGACCCGAACTCGTGGCGCAACATC	583				
QY	421	GAAATCGCAAGGCGCTGACTCTTTCATACCGTACCGGCGCATTTGGTGGCGCGCTG	480				
DB	584	GAAATCGCAAGGCGCTGACTCTTTCATACCGTACCGGCGCATTTGGTGGCGCGCTG	643				
QY	481	AATTACCAACCTGCAAGGACATGATTTGCTGTGGACGACAGGCAATTCGGCGTGATG	540				
DB	644	AATTACCAACCTGCAAGGACATGATTTGCTGTGGACGACAGGCAATTCGGCGTGATG	703				
QY	541	ATGAACCAATTAACAGCGCGCAACCGCAATGGAACAAATACACTCGGTTTCGGTGTG	600				
DB	704	ATGAACCAATTAACAGCGCGCAACCGCAATGGAACAAATACACTCGGTTTCGGTGTG	763				
QY	601	AGCAACGCGCGTGATGTCGCTTTCGCTGATTCGCAACGTCGCGCTCATGAGACCCGA	660				
DB	764	AGCAACGCGCGTGATGTCGCTTTCGCTGATTCGCAACGTCGCGCTCATGAGACCCGA	823				
QY	661	AGCGCGGCGAGCGTGGCTATCCGCTAGAGGCTGTGGCAGCGAGCAATTAATCCGTGGT	720				
DB	824	AGCGCGGCGAGCGTGGCTATCCGCTAGAGGCTGTGGCAGCGAGCAATTAATCCGTGGT	883				
QY	721	TGCTACGCGGTATCCCTGATCCGCTCAAAACAAATACCAACTTCTTGGGTGAAGATT	780				
DB	884	TGCTACGCGGTATCCCTGATCCGCTCAAAACAAATACCAACTTCTTGGGTGAAGATT	943				
QY	781	GCTTATCAATCAACGACAGCACCGCATCGGCCCATCGTTTAAAGCGCAGCGGGCAT	840				
DB	944	GCTTATCAATCAACGACAGCACCGCATCGGCCCATCGTTTAAAGCGCAGCGGGCAT	1003				
QY	841	AATTACAGCA-TTGAAGAGTCTTATAACCTGACCGCTTCTTCTGGCGGAAGCGATGA	899				
DB	1004	AATTACAGCA-TTGAAGAGTCTTATAACCTGACCGCTTCTTCTGGCGGAAGCGATGA	1063				
QY	900	CGTAAACAGACGCGCAATGCCAATCTTTTACGAATGGAAGCTGTGATCAAAATGGCT	959				
DB	1064	CGTAAACAGACGCGCAATGCCAATCTTTTACGAATGGAAGCTGTGATCAAAATGGCT	1123				
QY	960	GTGCTCTTTGAAGCGGACTTCGATATCAGACCAACCAAGTGGCGGCTTAAACAA	1019				
DB	1124	GTGCTCTTTGAAGCGGACTTCGATATCAGACCAACCAAGTGGCGGCTTAAACAA	1183				
QY	1020	AGGCTCGTTCCCGACGGATTATTCACCTGGAGCGGCAACTATATCAGAAGATTGGA	1079				
DB	1184	AGGCTCGTTCCCGATGGATTATTCACCTGGAGCGGCAACTATATCAGAAGATTGGA	1243				
QY	1080	GAATATATACAAACCGCAGATGGAACACCGGATTAACAGTTTCTTTGCGGTATGACAG	1139				
DB	1244	CGAAATATACAAACCGCAGATGGAACACCGGATTAACAGTTTCTTTGCGGTATGACAG	1303				
QY	1140	CCAAACCGTTGCAACTGGGCGCCCAACATCGCTTGTGCTTAAACCTTTTCGCCAGTCGGCG	1199				
DB	1304	CCAAACCGTTGCAACTGGGCGCCCAACATCGCTTGTGCTTAAACCTTTTCGCCAGTCGGCG	1363				
QY	1200	TCAGTTTGAAACCTTAAACCGCGAGATTAATTTACTTCAGCGAAAGAGTATCCCGTACTAC	1259				
DB	1364	TCAGTTTGAAACCTTAAACCGCGAGATTAATTTACTTCAGCGAAAGAGTATCCCGTACTAC	1423				
QY	1260	CAGCTCGAATCAACACCCGCTGAAACCACTAAATATGTTTCTCAGTGTCTGATCAAT	1319				
DB	1424	CAGCTCGAATCAACACCCGCTGAAACCACTAAATATGTTTCTCAGTGTCTGATCAAT	1483				
QY	1320	CCAAATGGAACGAGGTTCAGCAGCGGTGAGATATCCGTTTACGATCATACCAAAATGAC	1379				
DB	1484	CCAAATGGAACGAGGTTCAGCAGCGGTGAGATATCCGTTTACGATCATACCAAAATGAC	1543				
QY	1380	GCCTCAGGAATTTGAATCCGAGTGTCTATGCTGTGACAAAAACACCGCTGACGCAATAC	1439				
DB	1544	GCCTCAGGAATTTGAATCCGAGTGTCTATGCTGTGACAAAAACACCGCTGACGCAATAC	1603				
QY	1440	TTATAAGGCTGGAGCGGATTTGCGGTTGGCGCGCAACTGAATCAGGCTTGGCATGT	1499				
DB	1604	TTATAAGGCTGGAGCGGATTTGCGGTTGGCGCGCAACTGAATCAGGCTTGGCATGT	1663				
QY	1500	CGGTTACGACATTAATCTCCGCTACCGGTGCCCCAATCGCTCCGAAAGTGTATTTCACTTA	1559				
DB	1664	CGGTTACGACATTAATCTCCGCTACCGGTGCCCCAATCGCTCCGAAAGTGTATTTCACTTA	1723				
QY	1560	CAACCACTTACCGCAACTTTGCTGTAAGAGCAGAAAGTGTGATGACAGCGGCGATGCGG	1739				
DB	1724	CAACCACTTACCGCAACTTTGCTGTAAGAGCAGAAAGTGTGATGACAGCGGCGATGCGG	1793				
QY	1620	CCACACCTGTCTGCGAAGCGCGGCAAGAGTGTGATGACAGCGGCGATGCGG	1903				
DB	1784	CCACACCTGTCTGCGAAGCGCGGCAAGAGTGTGATGACAGCGGCGATGCGG	1843				
QY	1680	AAACAAATTTACCGCAACTTTGCTGTAAGAGCAGAAAGTGTGATGACAGCGGCGATGCGG	1739				
DB	1844	AAACAAATTTACCGCAACTTTGCTGTAAGAGCAGAAAGTGTGATGACAGCGGCGATGCGG	1903				
QY	1740	CTGTACTCAGATGAATTAATCTACTAGGTAATGCTGTAAGCAATCTTATCCGAAAAACCGGA	1799				
DB	1904	CTGTACTCAGATGAATTAATCTACTAGGTAATGCTGTAAGCAATCTTATCCGAAAAACCGGA	1963				
QY	1800	ATGCGAGATGCAAAATATCGATAGGCGCGAATCCGTTGCTTGGATGACAGCGCGCT	1859				
DB	1964	ATGCGAGATGCAAAATATCGATAGGCGCGAATCCGTTGCTTGGATGACAGCGCGCT	2023				
QY	1860	GAAATGCAAAAGTAGGCTCTTTGCTGAGGCTGGAATTTGTTCCGCTCGCTGGG	1919				
DB	2024	GAAATGCAAAAGTAGGCTCTTTGCTGAGGCTGGAATTTGTTCCGCTCGCTGGG	2083				
QY	1920	TTATGCGAAAAAGCAAACTGTGCGGCGCAACAGCGCTGTCTCCACAGCGCGCCGAAAGT	1979				
DB	2084	TTATGCGAAAAAGCAAACTGTGCGGCGCAACAGCGCTGTCTCCACAGCGCGCCGAAAGT	2143				
QY	1980	GATTGCGGCTGCACTACGAAAGCGCGGCAAAATGGGGTGTGTTCTCCGCGCTGAC	2039				
DB	2144	GATTGCGGCTGCACTACGAAAGCGCGGCAAAATGGGGTGTGTTCTCCGCGCTGAC	2203				
QY	2040	TTATCTGGGTGCGAAAAAGGCAAGAGCGCAATACACCGTTTATGAAAAACAGGGCGG	2099				
DB	2204	TTATCTGGGTGCGAAAAAGGCAAGAGCGCAATACACCGTTTATGAAAAACAGGGCGG	2263				
QY	2100	GGGTACGCTTTTGCAAAAAAGGTAAAGATTACCGGTGGCTGAAACAGTCCGCTTATGT	2159				





Query Match 23.9%; Score 1003; DB 2; Length 209;  
 Best Local Similarity 94.7%; Pred. No. 4.2e-56;  
 Matches 198; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKPLHMLPIAALVGSIFGNFVLADEAAATETTPVKAIEKEVRVKDQLNAPATVERVNLGR 60  
 DB 1 MKPLQMLPIAALVGSIFGNFVLADEAAATETTPVKAIEKAVRVKGQNPAPAAVERVNLNR 60

QY 61 TQEMIRNOKLVRYSTDVGLSDSRGHQKGFPAVRGVEGNRVGVSDGVSLPDSEENSLYA 120  
 DB 61 TQEMIRNOKLVRYSTDVGLSDSRGHQKGFPAVRGVEGNRVGVSDGVNLPDSEENSLYA 120

QY 121 RYGNFNSRLSTDPELVNRIETAKGADSFNTGSGALGGVNYQTQGHDLILLDDRRQFGVM 180  
 DB 121 RYGNFNSRLSTDPELVNRIETAKGADSFNTGSGALGGVNYQTQGHDLILLDDRRQFGVM 180

QY 181 MKNGYSSRNREWTNTLFGVSNDRVDAAL 209  
 DB 181 MKNGYSTRNREWTNTLFGVSNDRVDAAL 209

## RESULT 9

Q8GB30 PRELIMINARY; PRT; 763 AA.  
 ID Q8GB30; AC Q8GB30;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Transferrin-binding protein A.  
 GN Name=tbpa;  
 OS Haemophilus somnus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Histophilus.  
 OX NCBI\_TaxID=731;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=649;  
 RA Ekins A., Bahrami P., Sijercic A., Maret D., Niven D.F.;  
 RT "Haemophilus somnus possesses two systems for acquisition of  
 transferrin-bound iron."  
 RL J. Bacteriol. 186:4407-4411(2004).  
 DR EMBL; AY184230; AAC11733.1; -.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0005215; P:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR010948; TonB\_hemlactins.  
 DR TIGRFAMs; TIGR01786; TonB-hemlactins; 1.  
 DR TIGRFAMs; TIGR01776; TonB-tbp-lbp; 1.  
 SQ SEQUENCE 763 AA; 86642 MW; 9C339A449699EDD3 CRC64;

Query Match 20.4%; Score 857; DB 2; Length 763;  
 Best Local Similarity 30.2%; Pred. No. 5.2e-46;  
 Matches 242; Conservative 151; Mismatches 321; Indels 86; Gaps 28;

QY 20 PVLA-ADEAATETTPVKAIEKEVRVKDQLNAPATVERV-----NLGRTOQMIRNOKLV 73  
 DB 21 PALSADNSQEKTKPKAB-----ELGEISVVYANVEPIFSSQSEQLRKNMYSNERDLF 75

QY 74 RYSTVDGLSDSRH-QKGFPAVRGVEGNRVGVSDGVSLPDSEN-SLVARY-----GNF 125  
 DB 76 RHEVGIVPEGGRSGNGFAIGVDKRVAVIVDGI--PQASTMTSTSRYSSTERHNGNI 133

QY 126 NSRLSIDPELVNRIETAKGADSFNTGSGALGGVNYQTQGHDLILLDDRRQFGVMKNGY 185  
 DB 134 NNT-----EYENISSVKQKGVNMGSGALGGVSTTKETDFVPEPDRTEGFLSKTG 189

QY 186 SRNREWTNTLFGVSNDRVDAALYSQRGHETESAGERGYPVEGSGALIRGSSRGI 245  
 DB 190 TSKNREWRQVGGFKTRDFFGFAQLTKRWGHTINNGK-----GADITGFGRGK 239

QY 246 PDPKHKYHNFELGKIAYQINDKHRIGPSFNGQOQHNYTIESSYNLTASSWREADDVNRRR 305  
 DB 240 PNPISYHTTSLTKIGYDINNTHFTLEDBRAEKKFTTEKTLGLSDEN-REATDRTPYR 298

QY 306 NANLFYEWTSPDSNLSLKADFDYQ-TTKVAANNKGSFFDPTDYSTWTNNYQKDLNIYN 364  
 DB 299 RYGLEIRYN-GLSWLETAKEVAKQKIBQLSALRGISSY-----NNNLFQLAS-YQ 347

QY 365 RSMTRFKRFTLRWDSOPLQL-GGQHRLSLTKFASREFENLRDDYVFSERSVSTTSI 423  
 DB 348 YIQDTITRGL--STYPLALWRTHTRUSSKVEPRDQFLENSQRYFVYLMKKRPNY 405

QY 424 QH--PVKTYNTGFSLDQIOMNDVFSSRADIRYDHTKMTPOELNAEACHADCKTPPAAN-T 480  
 DB 406 TEVVPKSRIFSLSLDEVALTDITLKATIGGRYDRYNAPQNVTKTLGAKINFPSRKL 465

QY 481 YKWSGFGVGLAAQNAQMHVGYDITSGYRVNASEVYTYNHGSGN--WLPNPNLKAERS 538  
 DB 466 HLSWQ--LGLEYQVHPHQIGYRLSTGPRVPAEDLYFVSRSESTDIETIPNPFLOPETA 523

QY 539 THTLSLQGRSEKGTLDANLYQNNYRNFELSEQKLTTSQDVGCTQMNYYGMCSPYSEK 598  
 DB 524 LNHELTYPQNYAHFSGVGLFRTYHNFQIRER-----CKNRFWDPPDKSYGAK 575

QY 599 PEW-----QMNIDKARIRGLTGLNVTKVASFVPEG--WKLFGSLGYAKSLSGDMSL 652  
 DB 576 CTHSLAQFVNEPKAVIKGIEVSGAVNGS--AFGLSDGLTFRLKGS--YSKQNHGDGDL 631

QY 653 LSTPPKVIAGDYSPSEKGVFSRLTYLGAKAKADQYTYENKGRGTPLQKKVQDP 712  
 DB 632 KSIQFPTVVGIDYE--TEKWSISLTGRYSAAKAKADAETET-----THDKKVVQWMP 683

QY 713 WLKNSAYVDMYGVFKLAKNLTLAGVNVNVRKVTWDSLRGLYS--YSTNAVDRDGK 770  
 DB 684 FLSFSYFVVDLTGQVNLKSNVILNMGIFNLFRNTTWDSDAYNLFTRGFTSRVLKNQPS 743

QY 771 GLDRYASGRNYAVSLDWKF 790  
 DB 744 GINRTAPKRNFAASVEVRF 763

RESULT 10  
 Q934H9 PRELIMINARY; PRT; 759 AA.  
 ID Q934H9; AC Q934H9;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Transferrin binding protein A.  
 GN Name=tbpa;  
 OS Haemophilus somnus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Histophilus.  
 OX NCBI\_TaxID=731;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9L;  
 RX MEDLINE=21945385; PubMed=11948169;  
 DOI=10.1128/JB.184.9.2539-2542.2002;  
 RA Ekins A., Niven D.F.;  
 RT "Identification of fur and fldA homologs and a Pasteurella multocida  
 tbpA homolog in Histophilus ovis and effects of iron availability on  
 their transcription."  
 RL J. Bacteriol. 184:2539-2542(2002).  
 DR EMBL; AY040784; AAK68653.1; -.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0005215; P:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR010948; Lcfr/trsfrecept.  
 DR InterPro; IPR010949; TonB\_hemlactins.  
 DR TIGRFAMs; TIGR01786; TonB-hemlactins; 1.  
 DR TIGRFAMs; TIGR01776; TonB-tbp-lbp; 1.

DR	InterPro; IPR010917; TonB recept C.	
DR	TIGRFAMs; TIGR01786; TonB-hemolysin 1.	
DR	PROSITE; PS01156; TONB DEPENDENT REC_2; UNKNOWN_1.	
KW	Complete proteome; Hypothetical protein.	
SQ	SEQUENCE 784 AA; 89543 MW; FAC104265463FB2D CRC64;	
Query Match	45.9%; Score 1927; DB 2; Length 784;	
Best Local Similarity	48.1%; Pred. No. 3.4e-114;	
Matches	385; Conservative 135; Mismatches 202; Indels 78; Gaps 14;	
Qy	28 ATETTPVKAIEKVRVKDQLNAPA-----TVERVNLGRIQOEMIRNDKDLVRYSTDVGLS 82	
Db	26 AQETT-----ELEQITVQESATAEVNKTSPVTSKATIQEMVRDRLVRYTDDVGIS 81	
Qy	83 DSGRHQKFAVRGVEGVRGVSIDGSLPDSSENSLYARYGNFNSLSLSDPELVNRIE 142	
Db	82 DNGRFLKFAVRGVEDNRVGISIDGSLPDSSENSLYARYGNFNSLSLSDPELIQIDI 141	
Qy	143 AKGADSFNTGSLGGGVNTLTQGHDLDDRFQVMMKNGYSSRNREWTNTLFGVSN 202	
Db	142 VRGSDSFNAGSGLGGGVNTLDPQHVIVAGNSVGLALRGSVASKNREWRTLIGYVG 201	
Qy	203 DRVDAALLYSORGHETESAGERGVPEGAGSGAIIKRGSRGIPDPKSKHKHFLGKIAY 262	
Db	202 EKFDALLMYSQRTGHEFKS-----RSGPPEFRYSSQHPDPVTQRFHNYLAKNY 251	
Qy	263 QINDKHRIGPSFNGQGHNTTIESYNLTASSREADDVNRNANLFYEWTPDSNWLSS 322	
Db	252 QINDNQRIQTLNGQTGRVIDERSYTLGMSQWREADDQERLNANDYIYASTGLAY 311	
Qy	323 LKADFDYQTTKVAANNKGS--FPTDYSTWTRNYNQDLENIYNSMDTKFRTFLRMS 380	
Db	312 SKFDLDYQKDLAAVYKGGHFTD-----AKELNEIYDRMKTVFTRGSELNA 362	
Qy	381 QPQLGQGHRLSLKTFASRREFENLNDYDFSERVSRTS-----SIQHPKVTNYG 433	
Db	363 QPVHFGYHEHTLTIGYVSQSDFKINQD-----RIGIGTNYDTQVHTTYQPIRTKQY 416	
Qy	434 FSLSDQIOWNDVFSSRADIRYDHTMTQPELNAEC-HAC-DKTPPAANTYKWSGFGVLA 491	
Db	417 LSLKDHVRWMDTFSSHGLRYDHTLKLAPKELNAPCSKACLEBKPKPRTSTVTFAGLE 476	
Qy	492 AQLNQAHVGYDITSGYRVFNASEVFTYNHSGNMLPNPNLKAERSTHTLSIQGRSEK 551	
Db	477 AQLSPSWMLGVNISTGYRVFTASEMFFFTNAYGTWKSNSLPKPEKSNHTLSLKGNSK 536	
Qy	552 GTLDANLYQNNRYNFLSEOKLTTSGDVGTQOMNYYYGMCNPNYS-EKPEWQMONDKAR 610	
Db	537 GLLDLTLYQTYRHFLEQESL-----IQRTEMRY-----GRPTYQSQEQMVNLDKAK 586	
Qy	611 IRGLELTGRNLVTKVASFVPEGMKLFGLGKYSKLSGDNLSLSTQPPKVIAGVDYESPS 670	
Db	587 IYGVELTHVNLDQMIYAVIPQGFYALGYSKLSNNASLSIQPLKIILGLDYBATN 646	
Qy	671 EKMGVFSRLTYLGAKKAKDAQTYVYENKRGRT-----PLQKVKVD 710	
Db	647 GKWAIFNLRYLGEKRSADAK--VYEIKRRTERTVETDPTWQQTITRCKRELYPDLST 704	
Qy	711 YPMLNKSAFYVDFMGVFKYLAUNLTLRAGVNVNVRKTTWDSRLGLYSYSTTNAVDRDGK 770	
Db	705 YKHLNKSAFYVDFMGVFKYLAUNLTLRAGVNVNVRKTTWDSRLGLYSYSTTNAVDRDGK 764	
Qy	771 GLDVRASGRNYAVSLDWKF 790	
Db	765 GLQRFYAPGRNYAASLEIRF 784	
RESULT 7		
ID	P72073	
AC	P72073; PRELIMINARY; PRT; 296 AA.	
DT	01-FEB-1997 (TrEMBLrel. 02, Created)	
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)	

DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Hemoglobin receptor.	
GN	Name=hmbR;	
OS	Neisseria gonorrhoeae.	
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	
OC	Neisseriaceae; Neisseria.	
OX	NCBI_TaxID=485;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=MS11;	
RA	Stojiljkovic I., Larson J., Hwa V., Anic S., So M.;	
RL	Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; U40861; AAB18727.1; -	
DR	GO; GO:0019867; C:outer membrane; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0005215; F:transporter activity; IEA.	
DR	GO; GO:0006810; P:transport; IEA.	
KW	Receptor.	
SQ	SEQUENCE 296 AA; 32223 MW; 9520AE9B2A32947D CRC64;	
Query Match	34.8%; Score 1463; DB 2; Length 296;	
Best Local Similarity	39.8%; Pred. No. 3.2e-85;	
Matches	283; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 MKPLHMLPIAALVGSIFGNPVLAADEAAATETTPVKAIEKVRVKDQLNAPATVENVLGR 60	
Db	13 MKPLHMLPIAALVGSIFGNPVLAADEAAATETTPVKAIEKVRVKDQLNAPATVENVLGR 72	
Qy	61 IQQEMIRDNKDLVRYSTDVGLSDSGRHQKFAVRGVEGVRGVSIDGSLPDSSENSLYA 120	
Db	73 IQQEMIRDNKDLVRYSTDVGLSDSGRHQKFAVRGVEGVRGVSIDGSLPDSSENSLYA 132	
Qy	121 RYGNFNSSRLSIDPELVNRIEIAKGADSFNTGSGALGGGVNYOTLQGHDLDDRFQGVN 180	
Db	133 RYGNFNSSRLSIDPELVNRIEIAKGADSFNTGSGALGGGVNYOTLQGHDLDDRFQGVN 192	
Qy	181 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSORGHETESAGERGVPEGAGSGAIIIG 240	
Db	193 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSORGHETESAGERGVPEGAGSGANIRG 252	
Qy	241 SSRGIDPDPKSKHKHFLGKIAYQINDKHRIGPSFNGQGHNTT 284	
Db	253 SSRGIDPDPKSKHKHFLGKIAYQINDKHRIGPSFNGQGHNTT 296	
RESULT 8		
ID	Q9RGD8	
AC	Q9RGD8; PRELIMINARY; PRT; 209 AA.	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	HmbR (Fragment).	
GN	Name=hmbR;	
OS	Neisseria meningitidis.	
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	
OC	Neisseriaceae; Neisseria.	
OX	NCBI_TaxID=487;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=IR2855;	
RA	MedLINE=20096688; PubMed=10629191; DOI=10.1128/JB.182.2.439-447.2000;	
RA	Zhu W., Hunt D.J., Richardson A.R., Stojiljkovic I.;	
RT	"Use of Heme Compounds as Iron Sources by Pathogenic Neisseriae	
RT	requires the product of the hemo gene.";	
RL	J. Bacteriol. 182:439-447(2000).	
DR	EMBL; AFI33695; AAF24746.1; -	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0005215; F:transporter activity; IEA.	
DR	GO; GO:0006810; P:transport; IEA.	
FT	NON_TER 209 209	
SQ	SEQUENCE 209 AA; 22683 MW; DE5CD5FF0AD40759 CRC64;	

Db 361 DBIYNRMDSMTREKRIITRLDHPQLQGGRRHLSFKTFASRRDFENLNRDDYCFSGRVVR 420  
QY 419 TTSSIOHPVKTNTNYGFLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAA 478  
Db 421 TTSSIOHPVKTNTNYGFLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAA 480  
QY 479 NTYKMGSGFVGLAAQLNQAWHVGVDITSGYRVPNASEVFTYHNGSGNWLNPNLKAERS 538  
Db 481 NTYKMGSGFVGLAAQLNQAWHVGVDITSGYRVPNASEVFTYHNGSGNWLNPNLKAERS 540  
QY 539 THTLSLQGRSEKGTLDANLYQNNYRNFSEOKLTTSQDVGCTQNNYYGCMSPYSEK 598  
Db 541 THTLSLQGRSEKGTLDANLYQNNYRNFSEOKLTTSQDVGCTQNNYYGCMSPYSEK 600  
QY 599 PEMQONIDKARIRGLELGRNLNVKVASFVPEGWKLFGSLGYAKSKLSDGSLSLSTOPP 658  
Db 601 PEMQONIDKARIRGLELGRNLNVKVASFVPEGWKLFGSLGYAKSKLSDGSLSLSTOPP 660  
QY 659 KVIAGVDYESPSEKMGVFSRLTYLGAKKADQATYVYENKGRGTPLOKKVXDYPWLKNSA 718  
Db 661 KVIAGVDYESPSEKMGVFSRLTYLGAKKADQATYVYENKGRGTPLOKKVXDYPWLKNSA 720  
QY 719 YVDMYGFYKPAKNTLRAGVNVFNKRYTTWDSLRGLYSYSTTNAVDRDGLDRYRAS 778  
Db 721 YVDMYGFYKPAKNTLRAGVNVFNKRYTTWDSLRGLYSYSTTNAVDRDGLDRYRAS 780  
QY 779 GRNAYVSLDWKF 790  
Db 781 GRNAYVSLDWKF 792

RESULT 5  
P72085 PRELIMINARY; PRT; 791 AA.  
AC P72085  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hemoglobin receptor.  
GN Name=hmbR;  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Serogroup B;  
RA Stojiljkovic I., Larson J., Hwa V., Anic S., So M.;  
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U00860; AAB18729.1; -  
DR GO; GO:0019867; C:outer membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR010949; TonB hemolactins.  
DR TIGRFAMs; TIGR01786; TonB-hemolactins; 1.  
KW Receptor.  
SQ SEQUENCE 791 AA; 89281 MW; 12B957A15232B39C CRC64;

Query Match 87.3%; Score 3665.5; DB 2; Length 791;  
Best Local Similarity 86.9%; Pred. No. 5.2e-225;  
Matches 687; Conservative 44; Mismatches 59; Indels 1; Gaps 1;

QY 1 MKPLHMLPAAALVGSITFGNPLVADEAETTPVKAIEKVEVVKDOLNAPATVERVNLGR 60  
Db 1 MKPLHMLPAAALVGSITFGNPLVADEAETTPVKAIEKVEVVKDOLNAPATVERVNLGR 60  
QY 61 IQQEMIRNDKLVRYSTDVGLSDGRGHQKGFVRGVEGNVGVSDIGVSLPDSSENSLYA 120  
Db 61 IQQEMIRNDKLVRYSTDVGLSDGRGHQKGFVRGVEGNVGVSDIGVSLPDSSENSLYA 120  
QY 121 RYGNFNSSRLSIDPELVNRNIDIVKADSPNTGSGALGGGVNTQTQGRDLLLPERQFGVM 180

Db 121 RYGNFNSSRLSIDPELVNRNIDIVKADSPNTGSGALGGGVNTQTQGRDLLLPERQFGVM 180  
QY 181 MKNGYSSNRRENTNTLFGVSNDRVDAAALLYSQRGHETESAGRGYPVEGAGSGAI IRG 240  
Db 181 MKNGYSSNRRENTNTLFGVSNDRVDAAALLYSQRGHETESAGRGYPVEGAGSGAI IRG 240  
QY 241 SSRGIPDPSQKIKYHNFGLGKIAYQINDKRIQSPFNQGGHNYTIBESYNTLTASSWREADD 300  
Db 241 SARGIPDPSQKIKYHNFGLGKIAYQINDKRIQSPFNQGGHNYTIBESYNTLTASSWREADD 300  
QY 301 VNRRNANLFWBTPDPSQKIKYHNFGLGKIAYQINDKRIQSPFNQGGHNYTIBESYNTLTASSWREADD 360  
Db 301 VNRRNANLFWBTPDPSQKIKYHNFGLGKIAYQINDKRIQSPFNQGGHNYTIBESYNTLTASSWREADD 360  
QY 361 NIYNRSMDTRPKRFTLRMDSQQL- GGQHRLSLKTFFASRRREFENLNRDDYVFSRVSST 419  
Db 361 ELYNRSMDTRPKRFTLRMDSQQL- GGQHRLSLKTFFASRRREFENLNRDDYVFSRVSST 420  
QY 420 TSSIOHPVKTNTNYGFLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAA 479  
Db 421 TNSIOHPVKTNTNYGFLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAA 480  
QY 480 TYKMGSGFVGLAAQLNQAWHVGVDITSGYRVPNASEVFTYHNGSGNWLNPNLKAERS 539  
Db 481 TYKMGSGFVGLAAQLNQAWHVGVDITSGYRVPNASEVFTYHNGSGNWLNPNLKAERS 540  
QY 540 THTLSLQGRSEKGTLDANLYQNNYRNFSEOKLTTSQDVGCTQNNYYGCMSPYSEK 599  
Db 541 THTLSLQGRSEKGTLDANLYQNNYRNFSEOKLTTSQDVGCTQNNYYGCMSPYSEK 600  
QY 600 PEMQONIDKARIRGLELGRNLNVKVASFVPEGWKLFGSLGYAKSKLSDGSLSLSTOPP 659  
Db 601 DWQMNIDKARIRGLELGRNLNVKVASFVPEGWKLFGSLGYAKSKLSDGSLSLSTOPP 660  
QY 660 VIAGVDYESPSEKMGVFSRLTYLGAKKADQATYVYENKGRGTPLOKKVXDYPWLKNSAY 719  
Db 661 VIAGVDYESPSEKMGVFSRLTYLGAKKADQATYVYENKGRGTPLOKKVXDYPWLKNSAY 720  
QY 720 VFDYMGFYKPAKNTLRAGVNVFNKRYTTWDSLRGLYSYSTTNAVDRDGLDRYRAS 779  
Db 721 VFDYMGFYKPAKNTLRAGVNVFNKRYTTWDSLRGLYSYSTTNAVDRDGLDRYRAS 780  
QY 780 GRNAYVSLDWKF 790  
Db 781 GRNAYVSLDWKF 792

RESULT 6  
Q9CMS1 PRELIMINARY; PRT; 784 AA.  
ID Q9CMS1  
AC Q9CMS1; TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein PM0741.  
GN OrderedLocusNames=PM0741;  
OS Pasteurella multocida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Pasteurella.  
OX NCBI\_TaxID=747;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Pm70;  
RA MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;  
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;  
RT "Complete genomic sequence of Pasteurella multocida Pm70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
DR EMBL; AE006111; AAK02825.1; -  
DR GO; GO:0019867; C:outer membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR010949; TonB hemolactins.

```

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8013 clone 6;
RX MEDLINE=95302964; PubMed=7783623;
RA Stojiljkovic I., Hwa V., de Saint Martin L., O'Gaora P., Nassif X.,
RA Heffron F., So M.;
RT "The Neisseria meningitidis haemoglobin receptor: its role in iron
RT utilization and virulence.";
RL Mol. Microbiol. 15:531-541(1995).
DR EMBL; U18558; AAA80205.1; -.
DR PIR; S61335; S61335.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR010949; TonB hemolactrns.
DR TIGRFAMs; TIGR01786; TonB-hemolactrns; 1.
KW Receptor.
SQ SEQUENCE 792 AA; 89405 MW; 52381200297B37A2 CRC64;

Query Match 90.8%; Score 3812; DB 2; Length 792;
Best Local Similarity 91.2%; Pred. No. 2.4e-234;
Matches 722; Conservative 25; Mismatches 43; Indels 2; Gaps 2;

Qy 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAEIKVRVKDQNLNAPATVERVNLGR 60
Db 1 MKPLQMLPVAALVGSIFGNPVADEAATETTPVKAQVAVKVRKQGNAPAAVERVNLNR 60
Qy 61 IQEMIRDNKDLVRYSTDVGLSDSGRHQKGFVAVRVEGVRVGVSDVGLPDSSENSLYA 120
Db 61 IKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFVAVRVEGVRVGVSDVGLPDSSENSLYA 120
Qy 121 RYGNFNSRLSIDPELVNRNIDIVKGADSFNTGSGALGGVNYOTLQGHDLILLDDRQFGVM 180
Db 121 RYGNFNSRLSIDPELVNRNIDIVKGADSFNTGSGALGGVNYOTLQGHDLILLDDRQFGVM 180
Qy 181 MKNGYSRNRNREWTNTLFGVSNDRVDAALYSQRRGHETESAGRGYPVEGAGSAINRG 240
Db 181 MKNGYSTNRNREWTNTLFGVSNDRVDAALYSQRRGHETESAGRGYPVEGAGSAINRG 240
Qy 241 SSRGIPDPSPKHKNFLGKIAYQINDKHRIGPSFNGOQHNYTIEESYNLTASSWRADD 300
Db 241 SARGIPDPSPKHKNFLGKIAYQINDKHRIGPSFNGOQHNYTIEESYNLTASSWRADD 300
Qy 301 VNRNRNANLFYEWTPDNNWLSLKAQDYOTTKVAAVNNKGSFP-TDYSTWTRNYNOKDL 359
Db 301 VNRNRNANLFYEWTPDNNWLSLKAQDYOTTKVAAVNNKGSFP-TDYSTWTRNYNOKDL 359
Qy 360 ENIYNRSMDFRFRFTLRMDSPQLQ-LGGQHRISLKTFFASRRREFENLRDDYPSERSVR 418
Db 360 ENIYNRSMDFRFRFTLRMDSPQLQ-LGGQHRISLKTFFASRRREFENLRDDYPSERSVR 418
Qy 419 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRADIRYDHTKMTPOELNAEHCADKTPPAA 478
Db 419 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRADIRYDHTKMTPOELNAEHCADKTPPAA 478
Qy 421 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRAGIRYDHTKMTPOELNAEHCADKTPPAA 480
Db 421 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRAGIRYDHTKMTPOELNAEHCADKTPPAA 480
Qy 479 NTYKSGGFGVLAQLNQAHVGVYDITSGYRVPNASEVYFTYHNSGQNLNPNLKAERS 538
Db 479 NTYKSGGFGVLAQLNQAHVGVYDITSGYRVPNASEVYFTYHNSGQNLNPNLKAERS 538
Qy 539 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 598
Db 539 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 598
Qy 541 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 600
Db 541 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 600
Qy 599 PEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPP 658
Db 599 PEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPP 658
Qy 601 LEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPL 660
Db 601 LEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPL 660
Qy 659 KVIAGVDYESPSEKMGVFSRLTYLGAKKAKADAQYTVYENKRGTPFLQKVKDYPWLKNSA 718
Db 659 KVIAGVDYESPSEKMGVFSRLTYLGAKKAKADAQYTVYENKRGTPFLQKVKDYPWLKNSA 718

Db 661 KVIAGIDYESPSEKMGVFSRLTYLGAKKAKADAQYTVYENKMGTPFLQKVKDYPWLKNSA 720
Qy 719 YVFDMTGFPYKLAQNLTLRAGVYVFNRRKYTTWDSLRGLYSYSTNNAVDROGKGLDRVRAS 778
Db 721 YVFDMTGFPYKPVKNTLTLRAGVYVFNRRKYTTWDSLRGLYSYSTNNSVDRDGKGLDRVRAP 780
Qy 779 GRNVAVSLDWKF 790
Db 781 SRNVAVSLEWKF 792

RESULT 4
Q9RCGS9 PRELIMINARY; PRT; 792 AA.
ID Q9RCGS9
AC Q9RCGS9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hemoglobin receptor.
GN Name:hmbR;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DNM2;
RX MEDLINE=99291064; PubMed=10361300;
RA Lewis L.A., Gipson M., Hartman K., Ownbey T., Vaughn J., Dyer D.W.;
RT "Phase variation of HpuAB and HmbR, two distinct haemoglobin receptors
RT of Neisseria meningitidis DNM2.";
RL Mol. Microbiol. 32:977-989(1999).
DR EMBL; AF105339; AAF19056.1; -.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR010949; TonB hemolactrns.
DR TIGRFAMs; TIGR01786; TonB-hemolactrns; 1.
KW Receptor.
SQ SEQUENCE 792 AA; 89318 MW; CB64AC2D9649ABBA CRC64;

Query Match 90.5%; Score 3800; DB 2; Length 792;
Best Local Similarity 90.9%; Pred. No. 1.4e-233;
Matches 720; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAEIKVRVKDQNLNAPATVERVNLGR 60
Db 1 MKPLQMLPVAALVGSIFGNPVADEAATETTPVKAQVAVKVRKQGNAPAAVERVNLNR 60
Qy 61 IQEMIRDNKDLVRYSTDVGLSDSGRHQKGFVAVRVEGVRVGVSDVGLPDSSENSLYA 120
Db 61 IKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFVAVRVEGVRVGVSDVGLPDSSENSLYA 120
Qy 121 RYGNFNSRLSIDPELVNRNIDIVKGADSFNTGSGALGGVNYOTLQGHDLILLDDRQFGVM 180
Db 121 RYGNFNSRLSIDPELVNRNIDIVKGADSFNTGSGALGGVNYOTLQGHDLILLDDRQFGVM 180
Qy 181 MKNGYSRNRNREWTNTLFGVSNDRVDAALYSQRRGHETESAGRGYPVEGAGSAINRG 240
Db 181 MKNGYSTNRNREWTNTLFGVSNDRVDAALYSQRRGHETESAGRGYPVEGAGSAINRG 240
Qy 241 SSRGIPDPSPKHKNFLGKIAYQINDKHRIGPSFNGOQHNYTIEESYNLTASSWRADD 300
Db 241 SARGIPDPSPKHKNFLGKIAYQINDKHRIGPSFNGOQHNYTIEESYNLTASSWRADD 300
Qy 301 VNRNRNANLFYEWTPDNNWLSLKAQDYOTTKVAAVNNKGSFP-TDYSTWTRNYNOKDL 359
Db 301 VNRNRNANLFYEWTPDNNWLSLKAQDYOTTKVAAVNNKGSFP-TDYSTWTRNYNOKDL 359
Qy 360 ENIYNRSMDFRFRFTLRMDSPQLQ-LGGQHRISLKTFFASRRREFENLRDDYPSERSVR 418
Db 360 ENIYNRSMDFRFRFTLRMDSPQLQ-LGGQHRISLKTFFASRRREFENLRDDYPSERSVR 418
Qy 419 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRADIRYDHTKMTPOELNAEHCADKTPPAA 478
Db 419 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRADIRYDHTKMTPOELNAEHCADKTPPAA 478
Qy 421 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRAGIRYDHTKMTPOELNAEHCADKTPPAA 480
Db 421 TTSSIQHPVKTNTYGFSLDQIQNDVFSRRAGIRYDHTKMTPOELNAEHCADKTPPAA 480
Qy 479 NTYKSGGFGVLAQLNQAHVGVYDITSGYRVPNASEVYFTYHNSGQNLNPNLKAERS 538
Db 479 NTYKSGGFGVLAQLNQAHVGVYDITSGYRVPNASEVYFTYHNSGQNLNPNLKAERS 538
Qy 539 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 598
Db 539 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 598
Qy 541 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 600
Db 541 TTHTLSLQGRSEKGTLDANLYQNNYRNFLEEOKLTSGDVGCTQMYNYGMCSPYSEK 600
Qy 599 PEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPP 658
Db 599 PEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPP 658
Qy 601 LEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPL 660
Db 601 LEWQMONIDKARIGELTGLNVTYKASVPEEGWKLFGSLGYAKSLGSDNSLSTOPL 660
Qy 659 KVIAGVDYESPSEKMGVFSRLTYLGAKKAKADAQYTVYENKRGTPFLQKVKDYPWLKNSA 718
Db 659 KVIAGVDYESPSEKMGVFSRLTYLGAKKAKADAQYTVYENKRGTPFLQKVKDYPWLKNSA 718

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Db 121 RYGNFSSRLSDPELVRIEIVKGDSPNTSGALGGVNYQTQGRDLLDDRRQFGVM 180
QY 181 MKNGYSSRNREWTNTLFGVSNDRVDAAALYSQRRGHETESAGRGYPVEGAGSGAIRG 240
Db 181 MKNGYSTNRREWTNTLFGVSNDRVDAAALYSQRRGHETESAGRGYAVEGSGANIRG 240
QY 241 SSGGIPDPSPKHYHFLGKIAYQINDKHRIGPSFNGQQGHNTYTBESYNLTASSWREADD 300
Db 241 SARGIPDPSPKHYHFLGKIAYQINDKHRIGPSFNGQQGHNTYTBESYNLTASSWREADD 300
QY 301 VNRNRNANLFYEWTPDSNWLSSLKADFDYQTKVAAVNNKGSFPDMDYSTWTRNYNQKOLE 360
Db 301 VNRNRNANLFYEWTPDSNWLSSLKADFDYQTKVAAVNNKGSFPDMDYSTWTRNYNQKOLD 360
QY 361 NIYNRSMDFRFRFTLRMDSDIQL- GGOHRLSLKTFASRRFENLNDDYFYSERVST 419
Db 361 EYNRSMDFRFRFTLRMDSDIQL- GGOHRLSLKTFASRRFENLNDDYFYSERVST 420
QY 420 TSSIQHPVKTNYGFSLSQIQWINDVFSRRADIRYDHTKMTPOELNAEACHADCKTPPAAN 479
Db 421 TSSIQHPVKTNYGFSLSQIQWINDVFSRRADIRYDHTKMTPOELNAEACHADCKTPPAAN 480
QY 480 TYKGSFGVGLAAQLNQAHVGYDITSGYRVPNASEVYFTYNHSGSNLPLNPKAKERST 539
Db 481 TYKGSFGVGLAAQLNQAHVGYDITSGYRVPNASEVYFTYNHSGSNLPLNPKAKERST 540
QY 540 THTLSQGRSEKGTLDANLYQNNYRNFLESEOKLTTSGDVGCTQMNYYGCMSPYSEKP 599
Db 541 THTLSQGRSEKGTLDANLYQNNYRNFLESEOKLTTSGDVGCTQMNYYGCMSPYSEKP 600
QY 600 EQWONIDKARIRGLTGRNLNVTKVASFVPEGWKLFGLGAKKADQYTYVENKRGTPLOKKYKDYPLNKSAY 719
Db 601 DWQMKNIDKARIRGLTGRNLNVTKVASFVPEGWKLFGLGAKKADQYTYVENKRGTPLOKKYKDYPLNKSAY 720
QY 720 VFDMGYGFYKLAQNLTLRAGVYVFNKRYTTWDSLRGLYSYSTTNAVDRDCKGLDRYRAG 779
Db 721 VFDMGYGFYKLAQNLTLRAGVYVFNKRYTTWDSLRGLYSYSTTNAVDRDCKGLDRYRAG 780
QY 780 RNYAVSLDWKF 790
Db 781 RNYAVSLEWKF 791

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## RESULT 2

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P72084
ID P72084 PRELIMINARY; PRT; 791 AA.
AC P72084;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hemoglobin receptor.
GN Name=hmbR;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serogroup A;
RA Stojiljkovic I., Larson J., Hwa V., Anic S., So M.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U40859; AAB18728.1; -.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:004872; C:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR010949; TonB hemolactins.
DR TIGRFAMs; TIGR01786; TonB-hemolactins; 1.

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KW Receptor.
SQ SEQUENCE 791 AA; 89359 MW; A82C4721DCAAGED0 CRC64;
Query Match 90.9%; Score 3818.5; DB 2; Length 791;
Best Local Similarity 90.9%; Pred. No. 9.1e-235;
Matches 719; Conservative 25; Mismatches 46; Indels 1; Gaps 1;
QY 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAETKEVRVKDQLNAPATVERVNLGR 60
Db 1 MKPLQMLPIAALVGSIFGNPVLAADEAATETTPVKAETKAVRVKQORAPAAVERVNLNR 60
QY 61 IQQEMIRNDKOLVRYSTDVGLSDSGRHQKGFVAVRGVGNRVGVSIDGVSPLDSEENSLYA 120
Db 61 IQQEMIRNDKOLVRYSTDVGLSDSGRHQKGFVAVRGVGNRVGVSIDGVSPLDSEENSLYA 120
QY 121 RYGNFSSRLSDPELVRIEIVKGDSPNTSGALGGVNYQTQGRDLLDDRRQFGVM 180
Db 121 RYGNFSSRLSDPELVRIEIVKGDSPNTSGALGGVNYQTQGRDLLDDRRQFGVM 180
QY 181 MKNGYSSRNREWTNTLFGVSNDRVDAAALYSQRRGHETESAGRGYPVEGAGSGAIRG 240
Db 181 MKNGYSTNRREWTNTLFGVSNDRVDAAALYSQRRGHETESAGRGYPVEGAGSGAIRG 240
QY 241 SSGGIPDPSPKHYHFLGKIAYQINDKHRIGPSFNGQQGHNTYTBESYNLTASSWREADD 300
Db 241 SARGIPDPSPKHYHFLGKIAYQINDKHRIGPSFNGQQGHNTYTBESYNLTASSWREADD 300
QY 301 VNRNRNANLFYEWTPDSNWLSSLKADFDYQTKVAAVNNKGSFPDMDYSTWTRNYNQKOLE 360
Db 301 VNRNRNANLFYEWTPDSNWLSSLKADFDYQTKVAAVNNKGSFPDMDYSTWTRNYNQKOLE 360
QY 361 NIYNRSMDFRFRFTLRMDSDIQL- GGOHRLSLKTFASRRFENLNDDYFYSERVST 419
Db 361 EYNRSMDFRFRFTLRMDSDIQL- GGOHRLSLKTFASRRFENLNDDYFYSERVST 420
QY 420 TSSIQHPVKTNYGFSLSQIQWINDVFSRRADIRYDHTKMTPOELNAEACHADCKTPPAAN 479
Db 421 TSSIQHPVKTNYGFSLSQIQWINDVFSRRADIRYDHTKMTPOELNAEACHADCKTPPAAN 480
QY 480 TYKGSFGVGLAAQLNQAHVGYDITSGYRVPNASEVYFTYNHSGSNLPLNPKAKERST 539
Db 481 TYKGSFGVGLAAQLNQAHVGYDITSGYRVPNASEVYFTYNHSGSNLPLNPKAKERST 540
QY 540 THTLSQGRSEKGTLDANLYQNNYRNFLESEOKLTTSGDVGCTQMNYYGCMSPYSEKP 599
Db 541 THTLSQGRSEKGTLDANLYQNNYRNFLESEOKLTTSGDVGCTQMNYYGCMSPYSEKP 600
QY 600 EQWONIDKARIRGLTGRNLNVTKVASFVPEGWKLFGLGAKKADQYTYVENKRGTPLOKKYKDYPLNKSAY 719
Db 601 DWQMKNIDKARIRGLTGRNLNVTKVASFVPEGWKLFGLGAKKADQYTYVENKRGTPLOKKYKDYPLNKSAY 720
QY 720 VFDMGYGFYKLAQNLTLRAGVYVFNKRYTTWDSLRGLYSYSTTNAVDRDCKGLDRYRAG 779
Db 721 VFDMGYGFYKLAQNLTLRAGVYVFNKRYTTWDSLRGLYSYSTTNAVDRDCKGLDRYRAG 780
QY 780 RNYAVSLDWKF 790
Db 781 RNYAVSLEWKF 791

```

## RESULT 3

```

Q51104
ID Q51104 PRELIMINARY; PRT; 792 AA.
AC Q51104;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hemoglobin receptor.
GN Name=hmbR;

```

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3867.5	92.1	791	2	Q9JYA8	Q9JYA8 neisseria m
2	3818.5	90.9	791	2	P72084	P72084 neisseria m
3	3812	90.8	792	2	Q51104	Q51104 neisseria m
4	3800	90.5	792	2	Q9RGS9	Q9RGS9 neisseria m
5	3665.5	87.3	791	2	P72085	P72085 neisseria m
6	1927	45.9	784	2	Q9CWS1	Q9CWS1 pasteurella
7	1463	34.8	296	2	P72073	P72073 neisseria g
8	1003	23.9	209	2	Q9RGD8	Q9RGD8 neisseria m
9	857	20.4	763	2	Q8GB30	Q8GB30 haemophilus
10	854	20.3	759	2	Q934H9	Q934H9 haemophilus
11	850.5	20.2	760	2	Q934H8	Q934H8 haemophilus
12	833	19.8	777	2	Q9ALL8	Q9ALL8 pasteurella
13	827	19.7	777	2	Q83295	Q83295 pasteurella
14	792.5	18.9	972	1	HGBA_HAEIU	HGBA_HAEIU haemophilus
15	786.5	18.7	810	1	HPUB_NEIMA	HPUB_NEIMA neisseria m
16	786.5	18.7	810	1	HPUB_NEIMC	HPUB_NEIMC neisseria m
17	780.5	18.6	946	2	Q6JRV5	Q6JRV5 actinobacil
18	780.5	18.6	946	2	Q6JRV7	Q6JRV7 actinobacil
19	775.5	18.5	993	1	HGBC_HAEIN	HGBC_HAEIN haemophilus
20	772.5	18.4	948	2	Q84143	Q84143 actinobacil
21	767.5	18.3	1063	1	HGPI_HAEIN	HGPI_HAEIN haemophilus
22	767.5	18.3	1067	1	HGBB_HAEIN	HGBB_HAEIN haemophilus
23	766	18.2	1066	1	HGPC_HAEIN	HGPC_HAEIN haemophilus
24	759	18.1	1084	1	HGP3_HAEIN	HGP3_HAEIN haemophilus
25	755.5	18.0	1013	1	HGBA_HAEIN	HGBA_HAEIN haemophilus
26	753.5	17.9	967	2	Q9L6A7	Q9L6A7 pasteurella
27	752.5	17.9	999	1	HGP2_HAEIN	HGP2_HAEIN haemophilus
28	749	17.8	999	1	HGPB_HAEIN	HGPB_HAEIN haemophilus
29	745.5	17.8	1023	2	Q93326	Q93326 actinobacil
30	745.5	17.8	1023	2	Q93TF7	Q93TF7 actinobacil
31	743.5	17.7	1023	2	Q934C2	Q934C2 actinobacil



Db 361 EYNRSMDTRFKRFTLRDLSHPQLQGGRRHLSFKTFVSRDFENLRDDYFSGRVRT 420  
Qy 420 TSSIQHPVKTNYGFSLSDOIOWNDVFSRADIRYDHTKMTPOELNAEACHADCKTPPAAN 479  
Db 421 TSSIQHPVKTNYGFSLSDOIOWNDVFSRADIRYDHTKMTPOELNAEACHADCKTPPAAN 480  
Qy 480 TYKWSGFGVGLAAQLNAQWVGVDITSGYRVPNASEVFTYNHGSGNWLNPENLKAERST 539  
Db 481 TYKWSGFGVGLAAQLNAQWVGVDITSGYRVPNASEVFTYNHGSGNWLNPENLKAERST 540  
Qy 540 THTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSQDVCGTQNNYYGMCSPYSEKP 599  
Db 541 THTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSQDVCGTQNNYYGMCSPYSEKP 600  
Qy 600 ENQMONIDKARIRGELTGRNLNVTYKASFPVPEGWKLFGLSGYAKSKLSDNSLLSTQPK 659  
Db 601 ENQMONIDKARIRGELTGRNLNVTYKASFPVPEGWKLFGLSGYAKSKLSDNSLLSTQPK 660  
Qy 660 VIAGDYSPSEKMGVFSRLTYLGAKKADQYTVYENKGRGTPLQKKVKDYPWLNKSA 719  
Db 661 VIAGDYSPSEKMGVFSRLTYLGAKKADQYTVYENKGRGTPLQKKVKDYPWLNKSA 720  
Qy 720 VFDYMGFYKAKNLTLAGVYVNFNRKYTTWDSLRGLYSYSTTNVDRDCKGLDRYRAG 779  
Db 721 VFDYMGFYKAKNLTLAGVYVNFNRKYTTWDSLRGLYSYSTTNVDRDCKGLDRYRAG 780  
Qy 780 RNYAVSLDWKF 790  
Db 781 RNYAVSLEWKF 791

## RESULT 2

hemoglobin receptor precursor - Neisseria meningitidis  
C:Species: Neisseria meningitidis  
C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S61335  
R:Stojiljkovic, I.; Hwa, V.; de Saint Martin, L.; O'Gaora, P.; Nassif, X.; Heffron, F.; Mol. Microbiol. 15, 531-541, 1995  
A:Title: The Neisseria meningitidis haemoglobin receptor: its role in iron utilization  
A:Reference number: S61335; PMID:95302964; PMID:7783623  
A:Accession: S61335  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-792 <STO>  
A:Cross-references: UNIPROT:Q51104; EMBL:U18558; NID:G687639; PIDN:AAA80205.1; PID:G687639  
C:Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-792/Product: hemoglobin receptor #status predicted <MAT>  
F:68-206/Domain: tonB-dependent receptor amino-terminal homology <TNN>

Query Match 90.8%; Score 3812; DB 2; Length 792;  
Best Local Similarity 91.2%; Pred. No. 1.3e-242;  
Matches 722; Conservative 25; Mismatches 43; Indels 2; Gaps 2;

Qy 1 MKPLHMLPAAALVGSIFGNPVLAADEAATETTPVKAIEKVRVQDLNAPATVERVNLGR 60  
Db 1 MKPLHMLPAAALVGSIFGNPVLAADEAATETTPVKAIEKVRVQDLNAPATVERVNLGR 60  
Qy 61 IQQEMIRNDKLVRYSTDVGLSDSGRHKQGFVAVRVEGNRNVGSDIGVSLPDSSENSLYA 120  
Db 61 IQQEMIRNDKLVRYSTDVGLSDSGRHKQGFVAVRVEGNRNVGSDIGVSLPDSSENSLYA 120  
Qy 121 RYGNFNSSRLSDPELVNRNIEAKGADSFNTGSGALGGGVNTQTQGHDLDDRRQFGVM 180  
Db 121 RYGNFNSSRLSDPELVNRNIDIVKGDSPNTGSGALGGGVNTQTQGHDLDDRRQFGVM 180  
Qy 181 MKNGYSSRNREWTNTLFGVSDNRDVAALYSORRHETESAGERYPVEGAGSGAIRG 240  
Db 181 MKNGYSSRNREWTNTLFGVSDNRDVAALYSORRHETESAGERYPVEGAGSGAIRG 240  
Qy 241 SSRGIPDPSPKHYHNFGLGKIAYQINDKIRIGPSFNGQQGHNTYTBESYNLTASWREADD 300

Db 241 SARGIPDPSPKHYHNFGLGKIAYQINDKIRIGPSFNGQQGHNTYTBESYNLTASWREADD 300  
Qy 301 VNRNRNANLFWETTPDSNWLSSLKADPDYQTTKVAANVKNKSEF-TDYSTWTRVYNQDL 359  
Db 301 VNRNRNANLFWETTPDSNWLSSLKADPDYQTTKVAANVKNKSEF-TDYSTWTRVYNQDL 360  
Qy 360 ENIYNRSMDTRFKRFTLRDLSHPQLQGGRRHLSFKTFASRRDFENLRDDYFSGRVVR 418  
Db 361 ENIYNRSMDTRFKRFTLRDLSHPQLQGGRRHLSFKTFASRRDFENLRDDYFSGRVVR 420  
Qy 419 TSSIQHPVKTNYGFSLSDOIOWNDVFSRADIRYDHTKMTPOELNAEACHADCKTPPA 478  
Db 421 TSSIQHPVKTNYGFSLSDOIOWNDVFSRADIRYDHTKMTPOELNAEACHADCKTPPA 480  
Qy 479 NTYKWSGFGVGLAAQLNAQWVGVDITSGYRVPNASEVFTYNHGSGNWLNPENLKAERS 538  
Db 481 NTYKWSGFGVGLAAQLNAQWVGVDITSGYRVPNASEVFTYNHGSGNWLNPENLKAERS 540  
Qy 539 THTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSQDVCGTQNNYYGMCSPYSEK 598  
Db 541 THTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSQDVCGTQNNYYGMCSPYSEK 600  
Qy 599 PEWQMONIDKARIRGELTGRNLNVTYKASFPVPEGWKLFGLSGYAKSKLSDNSLLSTOPP 658  
Db 601 LEWQMONIDKARIRGELTGRNLNVTYKASFPVPEGWKLFGLSGYAKSKLSDNSLLSTOPP 660  
Qy 659 KVIAGDYSPSEKMGVFSRLTYLGAKKADQYTVYENKGRGTPLQKKVKDYPWLNKSA 718  
Db 661 KVIAGDYSPSEKMGVFSRLTYLGAKKADQYTVYENKGRGTPLQKKVKDYPWLNKSA 720  
Qy 719 YVDMYGFYKAKNLTLAGVYVNFNRKYTTWDSLRGLYSYSTTNVDRDCKGLDRYRAS 778  
Db 721 YVDMYGFYKAKNLTLAGVYVNFNRKYTTWDSLRGLYSYSTTNVDRDCKGLDRYRAS 780  
Qy 779 GRNVAVSLDWKF 790  
Db 781 SRNVAVSLDWKF 792

## RESULT 3

hemoglobin-haptoglobin-utilization protein NMA0474 [imported] - Neisseria meningitidis  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: A81965  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagsis, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; PMID:20222556; PMID:10761919  
A:Accession: A81965  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-810 <PAR>  
A:Cross-references: UNIPROT:Q9JWA2; GB:ALI62753; GB:ALI57959; NID:G7379120; PIDN:CAB83763  
C:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: hpuB; NMA0474

Query Match 18.7%; Score 786.5; DB 2; Length 810;  
Best Local Similarity 26.9%; Pred. No. 1.2e-43;  
Matches 232; Conservative 155; Mismatches 349; Indels 125; Gaps 29;

Qy 3 PLHMLPAAALVGSIFGNPVLAADEAATETTPVKAIEKVRVQDLNAPATVERVNLGR 57  
Db 2 PIPFPELVAAAIAQAQFAFAADPA-----PQSAQTLINEITVTGTHKQKLGEEKIRRT 56  
Qy 58 LGRIOEMIRNDKLVRYSTDVGLSDSGR-HQKGFVAVRVEGNRNVGSDIGVSLPDSSEEN 116  
Db 57 LDKL---LVNDEHDLVRYDPPGISVVEGGRAGSNGTIRGDKRVAINVDGLAQAESRS 113  
Qy 117 ---SLYARYGNFNSSRLSDPELVNRNIEAKGADSFNTGSGALGGGVNTQTQGHDL 172

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2005, 14:49:54 ; Search time 43 Seconds  
(without alignments)  
1767.703 Million cell updates/sec

Title: US-09-665-358-8  
Perfect score: 4200  
Sequence: 1 MKPLHMLPIAALVGSIFGNP.....GLDRYASGRNYAVSLDWKF 790

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3867.5	92.1	791	2 F81056	hemoglobin recepto
2	3812	90.8	792	2 S61335	hemoglobin recepto
3	786.5	18.7	810	2 A81965	hemoglobin-naptog
4	759	18.1	1084	2 B64088	hemoglobin-binding
5	714.5	17.0	953	2 B64083	hemoglobin-binding
6	706.5	16.8	764	2 H83055	probable outer mem
7	685.5	16.3	944	2 C81798	lactoferrin bindin
8	681.5	15.8	943	2 G81070	lactoferrin-bindin
9	649	15.5	698	2 B82443	heme transport pro
10	641	15.3	940	2 S49087	lactoferrin bindin
11	640	15.2	931	2 S66574	transferrin-bindin
12	597.5	14.2	911	2 S70911	transferrin-bindin
13	590	14.0	914	2 S70906	transferrin-bindin
14	588	14.0	910	2 C81832	transferrin-bindin
15	587.5	14.0	911	2 JN0821	transferrin-bindin
16	582	13.9	908	2 JN0819	transferrin-bindin
17	577	13.7	912	2 S70901	transferrin-bindin
18	576.5	13.7	915	2 F81196	transferrin-bindin
19	575	13.7	912	2 C64107	transferrin-bindin
20	562.5	13.4	915	2 A43335	transferrin-bindin
21	542	12.9	877	2 AC2211	heme transport pro
22	521.5	12.4	802	2 AC2075	outer membrane hem
23	481	11.5	758	2 I64084	hemoglobin recepto
24	460.5	11.0	733	2 A87521	TonB-dependent rec
25	447	10.6	766	2 A82857	outer membrane hem
26	447	10.6	766	2 D97634	probable outer mem
27	443	10.5	518	2 A64130	hypothetical prote
28	345.5	8.2	659	2 G91009	colicin I receptor
29	341.5	8.1	659	2 A85854	hypothetical prote

30	341	8.1	830	2 AH0477	probable TonB depe
31	337.5	8.0	663	1 QREIC	colicin I receptor
32	336.5	8.0	663	2 AG0782	colicin I receptor
33	323	7.7	725	2 A57148	outer membrane pro
34	322.5	7.7	851	2 A83484	probable heme util
35	313	7.5	723	2 C64058	outer membrane pro
36	307	7.3	751	2 AC0574	ferrienterobactin
37	304	7.2	713	2 F82506	probable TonB syst
38	300	7.1	665	2 AD0160	probable outer mem
39	299	7.1	784	2 D82437	TonB receptor-rela
40	297.5	7.1	702	2 AF3038	exogenous ferric s
41	297.5	7.1	707	2 E98247	outer membrane pro
42	293	7.0	660	2 D91176	heme utilization/t
43	293	7.0	660	2 E86022	outer membrane hem
44	293	7.0	696	2 H90798	Iha adhesin (impor
45	293	7.0	696	2 G85607	probable receptor

ALIGNMENTS

RESULT 1

F81056

hemoglobin receptor NMB1668 [imported] - Neisseria meningitidis (strain MC58 serogroup E  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: F81056  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizzia, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve.  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; UID:20175755; PMID:10710307  
A;Accession: F81056

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-791 <FET>  
A;Cross-references: UNIPROT:Q9JYA8; GB:AE002517; GB:AB002098; NID:G7226912; PIDN:AAF4201  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB1668  
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homology

Query Match	92.1%	Score 3867.5;	DB 2;	Length 791;
Best Local Similarity	92.3%	Pred. No. 3e-246;		
Matches 730;	Conservative 20;	Mismatches 40;	Indels 1;	Gaps 1;
Qy	1	MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAEIKVVRVKDQNLNAPATVRRVNLGR	60	
Db	1	MKPLQMLPIAALVGSIFGNPVLAADEAATETTPVKAEIKAVRVKQRPAAVRRVNLNR	60	
Qy	61	IQQEMIRDNKDIARYSTDVGLSDSGHKGFAVRGVGNEGVSDVSDVSLPDSSENSLYA	120	
Db	61	IKQEMIRDNKDIARYSTDVGLSDSGHKGFAVRGVGNEGVSDVSDVSLPDSSENSLYA	120	
Qy	121	RYGNFNSSRLSIDPELVRNIEIAKAGDSFNTGSGALGGGVNYQTLOGHLLDLDROQFGVM	180	
Db	121	RYGNFNSSRLSIDPELVRNIEIVKGADSFNTGSGALGGGVNYQTLOGHLLDLDROQFGVM	180	
Qy	181	MKNGYSRRNREWTNTLFGVSNDRVDAALYSQRRGHETESAGERGYFVGGSGALIRG	240	
Db	181	MKNGYSTNRNREWTNTLFGVSNDRVDAALYSQRRGHETESAGRGYAVGGSGANIRG	240	
Qy	241	SSRGIPDPSKHVHNFGLKIAYQINDKHRIQPSFNGQGHNYTTEESYNLTASSWREADD	300	
Db	241	SARGIPDSSKHVHNFGLKIAYQINDNHRIGASLNGQGHNYTTEESYNLTASSWREADD	300	
Qy	301	VNRRRNANLFYEWTPDPSNWLSSLKADPDYQTTKVAAVNNKGSFPTDYSTWTRNNQKDL	360	
Db	301	VNRRRNANLFYEWTPDPSNWLSSLKADPDYQTTKVAAVNNKGSFPMYDSTWTRNNQKDL	360	
Qy	361	NIYNRSMDTRFKFTLRMDSQPLQL-CGQHRLSLKTASRRREFENLRDDDYFSEVRSRT	419	

Db 541 THTLSLQGRGKGTDLNANLYQSNRYNRLSEBQNLTVSGTPGCTEDAYYYRCDPYKEKL 600  
QY 600 EWOMONIDKARIRGLTGLRLNVTYKASVFPVPEGWKLFGLGYAKSKLSDGNSLLSTQPPK 659  
Db 601 DWQMKNIDKARIRGLTGLRLNVDKVASVFPVPEGWKLFGLGYAKSKLSDGNSLLSTQPPK 660  
QY 660 VIAGVDYESPEKMGVFSRLTYLGAKKAKDAQYTYVYENKRGCTPQKKVKDYPWLNKSAY 719  
Db 661 VIAGIDYESPEKMGVFSRLTYLGAKKAKDAQYTYVYENKRGCTPQKKVKDYPWLNKSAY 720  
QY 720 VEDMYGFYKLAKNLTLRAGVYVFNRYKTYTWSLRGLYSYSTTNAVDRDCKGLDRIYRAG 779  
Db 721 VEDMYGFYKPAKNLTLRAGVYVFNRYKTYTWSLRGLYSYSTTNAVDRDCKGLDRIYRAG 780  
QY 780 RNYAVSLDWKF 790  
Db 781 RNYAVSLEWKF 791

RESULT 10  
US-08-537-361E-4  
; Sequence 4, Application US/08537361E  
; Patent No. 6121037  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nasasif, Xavier  
; TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor  
; NUMBER OF INVENTIONS: Genes and Uses  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/537,361E  
; FILING DATE: 02-OCT-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6121037han, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 94,784-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 791 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-537-361E-4

Query Match 87.3%; Score 3665.5; DB 3; Length 791;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 687; Conservative 44; Mismatches 59; Indels 1; Gaps 1;  
QY 1 MKPLHMLPIAALVGSIFGNPVLAADEAETTPVKAIEKVRVKDQLNAPATVERVNLGR 60  
Db 1 MKPLQWPPIAALLGSIFGNPVLAADEAETTPVKAIEKVRVKDQLNAPATVERVNLGR 60  
QY 61 IQQEMIRDNKDLVRYSTDVGLSDGRHQKGFPAVRGVEGNRVGSDVGLSDPSEENSLYA 120

Db 61 IQQEMIRDNKDLVRYSTDVGLSDGRHQKGFPAVRGVEGNRVGSDVGLSDPSEENSLYA 120  
QY 121 RYGNFNSSRLSIDPELVNRIETAKGADFNFTGSGALGGGVNYQTLOGHDLILLDDROFGVM 180  
Db 121 RYGNFNSSRLSIDPELVNRIETAKGADFNFTGSGALGGGVNYQTLOGHDLILLDDROFGVM 180  
QY 181 MKNGYSSRNRENTWTLGFGVSNDRVDAALLYSQRGHETESAGERGYPVEGAGSGAIIRG 240  
Db 181 MKNGYSTNRRENTWTLGFGVSNDRVDAALLYSQRGHETESAGERGYPVEGAGSGAIIRG 240  
QY 241 SSRGIPDPSKHYHNFGLKIAIYQINDKHRIGPSFNGQOQHNYTIEESNYLTASSHREADD 300  
Db 241 SARGIPDPSKHYHNFGLKIAIYQINDKHRIGPSFNGQOQHNYTIEESNYLTASSHREADD 300  
QY 301 VNRRNANLFYEWTPDPSNWLSSLKADFDYQTTKVAANVKNKGSFPPTDYSTWTNRYNOKOLE 360  
Db 301 VNRRNTNLFYEWTPDPSNWLSSLKADFDYQTTKVAANVKNKGSFPPTDYSTWTNRYNOKOLE 360  
QY 361 NIYNRSMDTRFKRFTLRMDSQPLQL-GGQHRLSLTKTFASRRREFENLRDDYFYSERVST 419  
Db 361 EYNSRMDTRFKRFTLRMDSHPLQLGGGRHRLSFKTFAGQORDFENLRDDYFYSERVST 420  
QY 420 TSSIOHPVKTNYGFSLSDOIQWINDVFSRADIRYDHTKMTPOELNAEACHADCKTPPAAN 479  
Db 421 TNSIOHPVKTNYGFSLSDOIQWINDVFSRADIRYDHTKMTPOELNAEACHADCKTPPAAN 480  
QY 480 TYKMGSGFVGLAAQLNQAHVGYDITSGYRVVPNASEVFTYVNHGSGNMLPNLKAERST 539  
Db 481 TYKMGSGFVGLAAQLNQAHVGYDITSGYRVVPNASEVFTYVNHGSGNMLPNLKAERST 540  
QY 540 THTLSLQGRGKGTDLNANLYQSNRYNRLSEBQNLTVSGTPGCTEDAYYYRCDPYKEKL 600  
Db 541 THTLSLQGRGKGTDLNANLYQSNRYNRLSEBQNLTVSGTPGCTEDAYYYRCDPYKEKL 600  
QY 600 EWOMONIDKARIRGLTGLRLNVTYKASVFPVPEGWKLFGLGYAKSKLSDGNSLLSTQPPK 659  
Db 601 DWQMKNIDKARIRGLTGLRLNVDKVASVFPVPEGWKLFGLGYAKSKLSDGNSLLSTQPPK 660  
QY 660 VIAGVDYESPEKMGVFSRLTYLGAKKAKDAQYTYVYENKRGCTPQKKVKDYPWLNKSAY 719  
Db 661 VIAGIDYESPEKMGVFSRLTYLGAKKAKDAQYTYVYENKRGCTPQKKVKDYPWLNKSAY 720  
QY 720 VEDMYGFYKLAKNLTLRAGVYVFNRYKTYTWSLRGLYSYSTTNAVDRDCKGLDRIYRAG 779  
Db 721 VEDMYGFYKPAKNLTLRAGVYVFNRYKTYTWSLRGLYSYSTTNAVDRDCKGLDRIYRAG 780  
QY 780 RNYAVSLDWKF 790  
Db 781 RNYAVSLEWKF 791

RESULT 11  
US-09-809-665A-32  
; Sequence 32, Application US/09809665A  
; Patent No. 6790950  
; GENERAL INFORMATION:  
; APPLICANT: Lowery E., David, et.al.  
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions  
; FILE REFERENCE: 28341/00435  
; CURRENT APPLICATION NUMBER: US/09/809,665A  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 60/153,453  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/128,689  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 09/545,199  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 967  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida

Best Local Similarity 90.9%; Pred. No. 0;  
Matches 720; Conservative 25; Mismatches 45; Indels 2; Gaps 2;  
Qy 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKEVRVKDQLNAPATVERVNLGR 60  
Db 1 MKPLQMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKAVRGQRNAPAAVERVNLNR 60  
Qy 61 IQQEMIRNDKLVRYSTDVGLSDSRHOKGFARVGEVNRVGVSDIGVSLPDSSENSLYA 120  
Db 61 IQQEMIRNDKLVRYSTDVGLSDSRHOKGFARVGEVNRVGVSDIGVSLPDSSENSLYA 120  
Qy 121 RYGNFNSRLSIDPELVNRIEIAKADSFNTGSGALGGVNYQTLQGHDLDDLDRQFGVM 180  
Db 121 RYGNFNSRLSIDPELVNRIEIAKADSFNTGSGALGGVNYQTLQGHDLDDLDRQFGVM 180  
Qy 181 MKNGYSRNREWTNTLGFVSNDRVDAALLYSORRGHETESAGRGYPVEGAGSAINRG 240  
Db 181 MKNGYSRNREWTNTLGFVSNDRVDAALLYSORRGHETESAGRGYPVEGAGSAINRG 240  
Qy 241 SSRGIPDPSKHYNFLGKIAYQINDKHRIKGFSPNGOQHNYTIEESYNLTASSWRADD 300  
Db 241 SARGIPDPSKHYNFLGKIAYQINDKHRIKGFSPNGOQHNYTIEESYNLTASSWRADD 300  
Qy 301 VRRRNANLFYEWTPDSNWLSSKADFDYQTKVAANNKGSFP-TDYSTWTRNYNQKDL 359  
Db 301 VRRRNANLFYEWTPDSNWLSSKADFDYQTKVAANNKGSFP-TDYSTWTRNYNQKDL 359  
Qy 360 ENIYNRSMDTRFKPTLRMDSDQIOL-GGQRLSLKTPASRRFENLRDYYFSERVSR 418  
Db 360 ENIYNRSMDTRFKPTLRMDSDQIOL-GGQRLSLKTPASRRFENLRDYYFSERVSR 418  
Qy 419 TTSSIQHPVKTNTYGFSLSDQIOWNDVPSRADIRYDHTKMTPOELNAEACHACDKTPAA 478  
Db 419 TTSSIQHPVKTNTYGFSLSDQIOWNDVPSRADIRYDHTKMTPOELNAEACHACDKTPAA 478  
Qy 479 NTYKWSGFVGLAAQLNOAHVGVYDITSGYRVPNASEVYFTYHNSGNGWLPNPNLKAERS 538  
Db 479 NTYKWSGFVGLAAQLNOAHVGVYDITSGYRVPNASEVYFTYHNSGNGWLPNPNLKAERS 538  
Qy 539 TTHTLSQLGRSEKTLTDANLYONRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 598  
Db 539 TTHTLSQLGRSEKTLTDANLYONRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 598  
Qy 599 PEWQONIDKARIRGLEITGRNLNTKVASFVPEGWKLFGLSGLYAKSLSGNSLLSTQPP 658  
Db 599 PEWQONIDKARIRGLEITGRNLNTKVASFVPEGWKLFGLSGLYAKSLSGNSLLSTQPP 658  
Qy 601 LEWQONIDKARIRGLEITGRNLNTKVASFVPEGWKLFGLSGLYAKSLSGNSLLSTQPP 660  
Db 601 LEWQONIDKARIRGLEITGRNLNTKVASFVPEGWKLFGLSGLYAKSLSGNSLLSTQPP 660  
Qy 659 KVIAGVDYESPEKGVFSRLTYLGAKKAKDAQYTVYENKGRGTPLOKVKDY PWNKSA 718  
Db 659 KVIAGVDYESPEKGVFSRLTYLGAKKAKDAQYTVYENKGRGTPLOKVKDY PWNKSA 718  
Qy 719 YVFDYGFYKLAUHLTRAGVYVFNRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 778  
Db 719 YVFDYGFYKLAUHLTRAGVYVFNRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 778  
Qy 721 YVFDYGFYKLAUHLTRAGVYVFNRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 780  
Db 721 YVFDYGFYKLAUHLTRAGVYVFNRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 780  
Qy 779 GRNVAVSLDWKF 790  
Db 779 GRNVAVSLDWKF 790  
Qy 781 SRNVAVSLEWKF 792  
Db 781 SRNVAVSLEWKF 792

RESULT 9  
US-08-817-707-4  
; Sequence 4, Application US/08817707  
; Patent No. 6277382  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor  
; TITLE OF INVENTION: Genes and Uses  
; NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,707  
FILING DATE: 19-AUG-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6277382nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 94,784-J  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 791 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-817-707-4

Query Match 87.3%; Score 3668.5; DB 3; Length 791;  
Best Local Similarity 87.0%; Pred. No. 0;  
Matches 688; Conservative 43; Mismatches 59; Indels 1; Gaps 1;  
Qy 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKEVRVKDQLNAPATVERVNLGR 60  
Db 1 MKPLQMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKAVRGQRNAPAAVERVNLNR 60  
Qy 61 IQQEMIRNDKLVRYSTDVGLSDSRHOKGFARVGEVNRVGVSDIGVSLPDSSENSLYA 120  
Db 61 IQQEMIRNDKLVRYSTDVGLSDSRHOKGFARVGEVNRVGVSDIGVSLPDSSENSLYA 120  
Qy 121 RYGNFNSRLSIDPELVNRIEIAKADSFNTGSGALGGVNYQTLQGHDLDDLDRQFGVM 180  
Db 121 RYGNFNSRLSIDPELVNRIEIAKADSFNTGSGALGGVNYQTLQGHDLDDLDRQFGVM 180  
Qy 181 MKNGYSRNREWTNTLGFVSNDRVDAALLYSORRGHETESAGRGYPVEGAGSAINRG 240  
Db 181 MKNGYSRNREWTNTLGFVSNDRVDAALLYSORRGHETESAGRGYPVEGAGSAINRG 240  
Qy 241 SSRGIPDPSKHYNFLGKIAYQINDKHRIKGFSPNGOQHNYTIEESYNLTASSWRADD 300  
Db 241 SARGIPDPSKHYNFLGKIAYQINDKHRIKGFSPNGOQHNYTIEESYNLTASSWRADD 300  
Qy 301 VRRRNANLFYEWTPDSNWLSSKADFDYQTKVAANNKGSFP-TDYSTWTRNYNQKDL 360  
Db 301 VRRRNANLFYEWTPDSNWLSSKADFDYQTKVAANNKGSFP-TDYSTWTRNYNQKDL 360  
Qy 361 NIYNRSMDTRFKPTLRMDSDQIOL-GGQRLSLKTPASRRFENLRDYYFSERVSR 419  
Db 361 NIYNRSMDTRFKPTLRMDSDQIOL-GGQRLSLKTPASRRFENLRDYYFSERVSR 419  
Qy 420 TSSIQHPVKTNTYGFSLSDQIOWNDVPSRADIRYDHTKMTPOELNAEACHACDKTPAA 479  
Db 420 TSSIQHPVKTNTYGFSLSDQIOWNDVPSRADIRYDHTKMTPOELNAEACHACDKTPAA 479  
Qy 480 TYKWSGFVGLAAQLNOAHVGVYDITSGYRVPNASEVYFTYHNSGNGWLPNPNLKAERS 539  
Db 480 TYKWSGFVGLAAQLNOAHVGVYDITSGYRVPNASEVYFTYHNSGNGWLPNPNLKAERS 539  
Qy 540 THTLSQGRSEKTLTDANLYONRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 599  
Db 540 THTLSQGRSEKTLTDANLYONRYNPLSEOKLTTSQDVGCTOMNYYYGMCNPNYSEK 599

GENERAL INFORMATION:  
APPLICANT: Stojiljkovic, Igor  
APPLICANT: So, Magdalene  
APPLICANT: Hwa, Vivian  
APPLICANT: Heffron, Fred  
APPLICANT: Nassif, Xavier  
TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor  
TITLE OF INVENTION: Genes and Uses  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,361E  
FILING DATE: 02-OCT-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6121037nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 94,784-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 792 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-361E-6

Query Match 90.5%; Score 3806; DB 3; Length 792;  
Best Local Similarity 91.2%; Pred. No. 0;  
Matches 722; Conservative 24; Mismatches 44; Indels 2; Gaps 2;  
QY 1 MKPLHMLPAAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKDQLNAPATVERVNLGR 60  
DB 1 MKPLQMLPAAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKDQLNAPATVERVNLGR 60  
QY 61 IQEIMIRDNDLVYSTDVLGSDSGRHKQGFVAVRGVGNRVSIDGVSPLDSEENSLYA 120  
DB 61 IQEIMIRDNDLVYSTDVLGSDSGRHKQGFVAVRGVGNRVSIDGVSPLDSEENSLYA 120  
QY 121 RYGNFNSSRLSDPELVRIETAKGADSFNTGSGALGGVNYQTLOCHDLLLDDRQFGVM 180  
DB 121 RYGNFNSSRLSDPELVRIETAKGADSFNTGSGALGGVNYQTLOCHDLLLDDRQFGVM 180  
QY 181 MNGYSRRNWTNTLFGVSDNRDVAALLYSORRHETESAGERYPVEGAGSGAIIRG 240  
DB 181 MNGYSRRNWTNTLFGVSDNRDVAALLYSORRHETESAGERYPVEGAGSGAINIRG 240  
QY 241 SARGIPDPSSKHVNFGLKIAQINDKHRIQSPFNGQQGHNTYIESYNTLTASSWREADD 300  
DB 241 SARGIPDPSSKHVNFGLKIAQINDKHRIQSPFNGQQGHNTYIESYNTLTASSWREADD 300  
QY 301 VNRERRNANLFYEWTPPSNWLSSLKADPDYQTTKVAANVNGSGFP-TDYSTWTRNYSKDL 359  
DB 301 VNRERRNANLFYEWTPPSNWLSSLKADPDYQTTKVAANVNGSGFP-TDYSTWTRNYSKDL 359  
QY 360 ENLYNRSMDTRFKFTLRMDSPQL-L-GGCHRLSLKTFASRRREFENLNRDDYFVSERVR 418  
DB 361 DELYNRSMDTRFKFTLRMDSPQL-L-GGCHRLSLKTFASRRREFENLNRDDYFVSERVR 418  
QY 419 TTSSIQHPVKTTNYGFSLSDDQIQWNVFSSRAGIRYDHTKMTPOELNAEACHADKTPPAA 478

Db 421 TTSSIQHPVKTTNYGFSLSDDQIQWNVFSSRAGIRYDHTKMTPOELNAEACHADKTPPAA 480  
QY 479 NTKYKWSGFGVGLAAQLNQAHWVGYDITSGYRVPNAASEVYFTYNHGSGNWLPNPNLKAERS 538  
Db 481 NTKYKWSGFGVGLAAQLNQAHWVGYDITSGYRVPNAASEVYFTYNHGSGNWLPNPNLKAERS 540  
QY 539 TTHTLTSLQORSEKGTLDANLYQNNYRNFLSEBQKLTTSQDVGCTQWNYYYGMCNPNYSEK 598  
Db 541 TTHTLTSLQORSEKGTLDANLYQNNYRNFLSEBQKLTTSQDVGCTQWNYYYGMCNPNYSEK 600  
QY 599 PEWQONIDKARIRGLELTGRNLNVTYKASFVPEGHKLFGLSLGYAKSLSGDNLSTQPP 658  
Db 601 LEWQONIDKARIRGLELTGRNLNVTYKASFVPEGHKLFGLSLGYAKSLSGDNLSTQPP 660  
QY 659 KVIAGVDYESPEKGVFSRLTYLGAKKAKDAQYTYENKGRGTPLOKKVKDYPWLNKSA 718  
Db 661 KVIAGIDYESPEKGVFSRLTYLGAKKAKDAQYTYENKGRGTPLOKKVKDYPWLNKSA 720  
QY 719 YVFDMYGFYKLAKNLTLAGVYVNFNRKYTTWDSLRGLYSYSTTNNAVDRDGKGLDRYRAS 778  
Db 721 YVFDMYGFYKPVKNLTLAGVYVNFNRKYTTWDSLRGLYSYSTTNNAVDRDGKGLDRYRAP 780  
QY 779 GRNYAVSLDWKF 790  
Db 781 SRNYAVSLEWKF 792

RESULT 8  
US-08-537-361E-2  
Sequence 2, Application US/08537361E  
Patent No. 6121037  
GENERAL INFORMATION:  
APPLICANT: Stojiljkovic, Igor  
APPLICANT: So, Magdalene  
APPLICANT: Hwa, Vivian  
APPLICANT: Heffron, Fred  
APPLICANT: Nassif, Xavier  
TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor  
TITLE OF INVENTION: Genes and Uses  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,361E  
FILING DATE: 02-OCT-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6121037nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 94,784-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 792 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-361E-2

Query Match 90.5%; Score 3799; DB 3; Length 792;





```
/ FILING DATE: 19-AUG-1997
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6277382han, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 94,784-J
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 792 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-817-707-2

Query Match          90.8%; Score 3814; DB 3; Length 792;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 723; Conservative 24; Mismatches 43; Indels 2; Gaps 2;

QY 1 MKPLHMLPTAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKQQLNAPATVERVNLGR 60
DB 1 MKPLQMLPTAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKQQLNAPATVERVNLNR 60

QY 61 IQQEMIRDNKDLVRYSTDVGLSDSGRHKQGFVAVRGVEGNRVGVSIDGVSLLPSEENSLYA 120
DB 61 IQQEMIRDNKDLVRYSTDVGLSDSGRHKQGFVAVRGVEGNRVGVSIDGVSLLPSEENSLYA 120

QY 121 RYGNFNSSRLSIDPELVARNIEIAKAGDSFNTGSGALGGGVNYQTLLQGHDLDDRRQFGVM 180
DB 121 RYGNFNSSRLSIDPELVARNIDIVKAGDSFNTGSGALGGGVNYQTLLQGRDLLLPERQFGVM 180

QY 181 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSQRRGHETESAGRGYPVEGAGSGAIRG 240
DB 181 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSQRRGHETESAGRGYPVEGAGSGANIRG 240

QY 241 SARGIPDPSPQHKYHNFGLKIAQINDKIRIGSPFNGQGHNTTIESYNLTASSWREADD 300
DB 241 SARGIPDPSPQHKYHNFGLKIAQINDKIRIGSPFNGQGHNTTIESYNLTASSWREADD 300

QY 301 VNRNRNANLFYEWTPDSNLSLKADFDYQTTKVAANNKSGSP-TDYSWTTRNTYKQDL 359
DB 301 VNRNRNANLFYEWTPDSNLSMKVADVDYQTKVSAVNYKGSFPFIEDSTLTFRNTYKQDL 360

QY 360 ENIYRSMOTRPFRTLRWDSQPLQ-GGQRLSLKTPASRRPEFENLNDRDDYFSEVRVR 418
DB 361 DEIYNRSMOTRPFRTLRWDSQPLQ-LGGGRHRLSPKTFASRRDPENLNDRDDYFSEGRVVR 420

QY 419 TTSSIQHPVKTNYGFSLSQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADKTPPAA 478
DB 421 TTSSIQHPVKTNYGFSLSQIQWNVDFSSRAGIRYDHTKMTPOELNAEACHADKTPPAA 480

QY 479 NTYKGSFGVGLAAQLNQAHVGYDITSGYRVPNASEVFTYHNGSGNWLNPNLKAERS 538
DB 481 NTYKGSFGVGLAAQLNQAHVGYDITSGYRVPNASEVFTYHNGSGNWLNPNLKAERT 540

QY 539 THTLSLQGRSEKGTLDANLYQNNYNFLSBEOKLTTSQDVGCTQNNYYGHCSPYSEK 598
DB 541 THTLSLQGRSEKGTLDANLYQNNYNFLSBEOKLTTSQDVGCTQNNYYGHCSPYSEK 600

QY 599 PEMQONIDKARIRGLTGRNLNVKVASFPVPGWKLFGSLGVAKSLSGDNLSTLSTQPP 658
DB 601 LEWQONIDKARIRGLTGRNLNVKVASFPVPGWKLFGSLGVAKSLSGDNLSTLSTQPL 660

QY 659 KVIAGVDYSPSKWGVFSLTYLGAQKADQYTYENKRGTPLOKVKDYDYPMLNKA 718
DB 661 KVIAGIDYSPSEKGVFSLTYLGAQKADQYTYENKRGTPLOKVKDYDYPMLNKA 720

QY 719 YPDMYGFYKLANLTLRAGVNVFNKRYTTWDSRLGLYSYSTTNNAVDRDGLDRYAS 778
DB 721 YPDMYGFYKLANLTLRAGVNVFNKRYTTWDSRLGLYSYSTTNNAVDRDGLDRYAP 780
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779 GRNVAVSLDWKF 790  
781 SRNVAVSLDWKF 792

RESULT 5  
US-08-326-670A-2  
Sequence 2, Application US/083266670A  
Patent No. 5698438  
GENERAL INFORMATION:  
APPLICANT: Stojiljkovic, Igor  
APPLICANT: SO, Magdalene  
APPLICANT: Hwa, Vivian  
APPLICANT: Heffron, Fred  
APPLICANT: Nassif, Xavier  
TITLE OF INVENTION: A No. 5698438el Bacterial Hemoglobin Receptor Gene and Uses  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegratti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/326,670A  
FILING DATE: 18 OCT 1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5698438han, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 94,784  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 810-221-8317  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 792 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-326-670A-2

Query Match 90.8%; Score 3812; DB 1; Length 792;  
Best Local Similarity 91.2%; Pred. No. 0;  
Matches 722; Conservative 25; Mismatches 43; Indels 2; Gaps 2;

QY 1 MKPLHMLPTAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKQQLNAPATVERVNLGR 60  
DB 1 MKPLQMLPTAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKQQLNAPATVERVNLNR 60

QY 61 IQQEMIRDNKDLVRYSTDVGLSDSGRHKQGFVAVRGVEGNRVGVSIDGVSLLPSEENSLYA 120  
DB 61 IQQEMIRDNKDLVRYSTDVGLSDSGRHKQGFVAVRGVEGNRVGVSIDGVSLLPSEENSLYA 120

QY 121 RYGNFNSSRLSIDPELVARNIEIAKAGDSFNTGSGALGGGVNYQTLLQGHDLDDRRQFGVM 180  
DB 121 RYGNFNSSRLSIDPELVARNIDIVKAGDSFNTGSGALGGGVNYQTLLQGRDLLLPERQFGVM 180

QY 181 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSQRRGHETESAGRGYPVEGAGSGAIRG 240  
DB 181 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSQRRGHETESAGRGYPVEGAGSGANIRG 240

QY 241 SARGIPDPSPQHKYHNFGLKIAQINDKIRIGSPFNGQGHNTTIESYNLTASSWREADD 300  
DB 241 SARGIPDPSPQHKYHNFGLKIAQINDKIRIGSPFNGQGHNTTIESYNLTASSWREADD 300

Qy 661 IAGVDYSPSEKMGVFSRLTYLGAKKADAQYTVYENKRGCTPQKKVKDYPWLNKSAVV 720  
Db 661 IAGIDYSPSEKMGVFSRLTYLGAKKADAQYTVYENKRGCTPQKKVKDYPWLNKSAVV 720  
Qy 721 FDMTGFYKLAQNLTLRAGVYVFNKRYTTWDSLRGLYSYSTTNAVDRDGKGLDRYASGR 780  
Db 721 FDMTGFYKLAQNLTLRAGVYVFNKRYTTWDSLRGLYSYSTTNAVDRDGKGLDRYASGR 780  
Qy 781 NYAVSLDWKF 790  
Db 781 NYAVSLDWKF 790  
RESULT 3  
US-08-990-470A-2  
; Sequence 2, Application US/08990470A  
; Patent No. 6123942  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6123942el Bacterial Hemoglobin Receptor  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/990,470A  
; APPLICATION NUMBER: US/08/990,470A  
; FILING DATE: 15-DEC-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6123942nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 94,784-K  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 792 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-990-470A-2  
Query Match 90.8%; Score 3814; DB 3; Length 792;  
Best Local Similarity 91.3%; Pred. No. 0;  
Matches 723; Conservative 24; Mismatches 43; Indels 2; Gaps 2;  
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Db 1 MKPLQMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKDQLNAPATVERVNLNR 60  
Qy 61 IQQEMIRNDKDLRYSTVDGLSDSGRHKQGFVAVRGVGNRNVGSIDGVSPLDSEENSLYA 120  
Db 61 IKQEMIRNDKDLRYSTVDGLSDSGRHKQGFVAVRGVGNRNVGSIDGVSPLDSEENSLYA 120  
Qy 121 RYGNFNSRLSIDPELVNRIEIAKADSFNTGSGALGGGVNYQTLOGHLLLDLDRQFGVM 180  
Db 121 RYGNFNSRLSIDPELVNRIEIAKADSFNTGSGALGGGVNYQTLOGHLLLDLDRQFGVM 180

Qy 181 MKNGYSRRNREWTNTLGFVSNDRVDAALYISORRHETESAGRGYPVEGAGSGAIRG 240  
Db 181 MKNGYSTNREWTNTLGFVSNDRVDAALYISORRHETESAGRGYPVEGAGSGANIRG 240  
Qy 241 SSRGIPDPSKHXYNFILKJAYQINDKRIQPSFNGOQHNYTTEESVNLTFASWREADD 300  
Db 241 SARGIPDPSKHXYNFILKJAYQINDKRIQPSFNGOQHNYTTEESVNLTFASWREADD 300  
Qy 301 VNRRNANLFYEWTPDGNLSSLKADPDYOTTKVAANVNGSGEP-TDYSTWTRVNNOKDL 359  
Db 301 VNRRNANLFYEWTPDGNLSSLKADPDYOTTKVAANVNGSGEP-TDYSTWTRVNNOKDL 360  
Qy 360 ENIYNRSMDFRFRFTLRMDSPQLQL-CGGHRLSLKTFASRRREFENLRDYYFSEVSR 418  
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Qy 419 TTSSIQHPVKTNTNYGFSLSQIQWNVFSSRADIRYDHTKMTPOELNAECHACDKTPPAA 478  
Db 421 TTSSIQHPVKTNTNYGFSLSQIQWNVFSSRADIRYDHTKMTPOELNAECHACDKTPPAA 480  
Qy 479 NTYKMGSGFVGLAAQLNAQWVGYDITSGYRVPNASEVYFTYHSGNWLNPNLKABERS 538  
Db 481 NTYKMGSGFVGLAAQLNAQWVGYDITSGYRVPNASEVYFTYHSGNWLNPNLKABERS 540  
Qy 539 TTHTLSLQGRSEKGTLDANLYQNNYRNFLESEOKLTTSGDVGCTQMNYVYGMCSNPYSEK 598  
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Qy 599 PEWQMONIDKARIRGLTGLRLNVTKVASFVPEGWKLFGLSGLYAKSLSGDNLSTQPP 658  
Db 601 LEWQMONIDKARIRGLTGLRLNVTKVASFVPEGWKLFGLSGLYAKSLSGDNLSTQPP 660  
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Db 721 YVFDYMGFYKLAQNLTLRAGVYVFNKRYTTWDSLRGLYSYSTTNAVDRDGKGLDRYAP 780  
Qy 779 GRNYAVSLDWKF 790  
Db 781 SRNYAVSLDWKF 792  
RESULT 4  
US-08-817-707-2  
; Sequence 2, Application US/08817707  
; Patent No. 6277382  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/817,707

Db 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKEVRVKDQNLNAPATVERVNLGR 60  
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Db 61 IQEMIRDNKDLVRYSTVDGLSDGRHOKGFAVRGVEGNRVGVSIDGVSIPSEENSLYA 120  
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Db 121 RYGNFNSSRLSDPELVRIEIAKAGADSFNTGSGALGGGVNTQTLQGHDLDDDDROFGVM 180  
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Db 181 MKNGYSRRNREWTNTLFGVSNDRVDAALYSORRGHETESAGERGYPVEGAGSGAIRG 240  
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Db 241 SSRGIPDPKSKHYHFLGKIAYQINDKHRIQSGFNGQOQHNTYIESYNTLTASSWREADD 300  
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Db 301 VNRRNANLFYEWTPDSNWLSSLKADFDYQTTKVAAVNNKGSFPPTDYSTWTRYNQKOLE 360  
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Db 361 NIYNRSMDFRFRFTLRMDSQPLQGGQHRLSLKTFASSRREFENLRDDYYFSERSVRTT 420  
QY 421 SSIQHPVKTTNYGFSLSDOIQWNVFSSRADIRYDHTKMTPOELNAECHACDKTPPAANT 480  
Db 421 SSIQHPVKTTNYGFSLSDOIQWNVFSSRADIRYDHTKMTPOELNAECHACDKTPPAANT 480  
QY 481 YKWSGFVGLAQLNAQAHVGYDITSGYRVPNASEVYFTYNNHSGGNWLPNPKLKAERSTT 540  
Db 481 YKWSGFVGLAQLNAQAHVGYDITSGYRVPNASEVYFTYNNHSGGNWLPNPKLKAERSTT 540  
QY 541 HTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSBGVGTOMNYYYGMCNPNYSEKPE 600  
Db 541 HTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSBGVGTOMNYYYGMCNPNYSEKPE 600  
QY 601 WQMONIDKARIRGLELTGRLNVTKVASFVPEGWKLFGLSLGYAKSKLSDGNSLLSTOPPKE 660  
Db 601 WQMONIDKARIRGLELTGRLNVTKVASFVPEGWKLFGLSLGYAKSKLSDGNSLLSTOPPKE 660

RESULT 2

US-08-537-361E-8  
; Sequence 8, Application US/08537361E  
; Patent No. 6121037  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor  
; TITLE OF INVENTION: Genes and Uses  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois

COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,361E  
FILING DATE: 02-OCT-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6121037nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 94,784-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 790 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-361E-8  
Query Match 99.3%; Score 4171; DB 3; Length 790;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 784; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
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Db 361 NIYNRSMDFRFRFTLRMDSQPLQGGQHRLSLKTFASSRREFENLRDDYYFSERSVRTT 420  
QY 421 SSIQHPVKTTNYGFSLSDOIQWNVFSSRADIRYDHTKMTPOELNAECHACDKTPPAANT 480  
Db 421 SSIQHPVKTTNYGFSLSDOIQWNVFSSRADIRYDHTKMTPOELNAECHACDKTPPAANT 480  
QY 481 YKWSGFVGLAQLNAQAHVGYDITSGYRVPNASEVYFTYNNHSGGNWLPNPKLKAERSTT 540  
Db 481 YKWSGFVGLAQLNAQAHVGYDITSGYRVPNASEVYFTYNNHSGGNWLPNPKLKAERSTT 540  
QY 541 HTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSBGVGTOMNYYYGMCNPNYSEKPE 600  
Db 541 HTLSLQGRSEKGTLDANLYQNNYRNFLEBEQKLTTSBGVGTOMNYYYGMCNPNYSEKPE 600  
QY 601 WQMONIDKARIRGLELTGRLNVTKVASFVPEGWKLFGLSLGYAKSKLSDGNSLLSTOPPKE 660  
Db 601 WQMONIDKARIRGLELTGRLNVTKVASFVPEGWKLFGLSLGYAKSKLSDGNSLLSTOPPKE 660

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 6, 2005, 14:49:54 ; Search time 43 Seconds  
(without alignments)  
1371.460 Million cell updates/sec

Title: US-09-665-358-8

Perfect score: 4200

Sequence: 1 MKPLHMLPIAALVGSIFGNP.....GLDRYASGRNRYAVSLDWKF 790

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4187	99.7	790	3	US-08-817-707-8
2	4171	99.3	790	3	US-08-537-361E-8
3	3814	90.8	792	3	US-08-990-470A-2
4	3814	90.8	792	3	US-08-817-707-2
5	3812	90.8	792	1	US-08-326-670A-2
6	3810	90.7	790	3	US-08-817-707-6
7	3806	90.6	792	3	US-08-537-361E-6
8	3799	90.5	792	3	US-08-817-707-4
9	3668.5	87.3	791	3	US-08-537-361E-4
10	3665.5	87.3	791	3	US-08-537-361E-4
11	753.5	17.9	967	4	US-09-809-665A-32
12	737.5	17.6	669	4	US-08-809-665A-105
13	702.5	16.7	789	4	US-09-252-991A-27011
14	666	15.9	944	2	US-08-867-941-24
15	666	15.9	944	3	US-09-074-658-24
16	651.5	15.5	944	2	US-08-867-941-23
17	651.5	15.5	944	3	US-09-074-658-23
18	642.5	15.3	971	3	US-08-405-728-2
19	641	15.3	941	3	US-09-074-658-75
20	640	15.2	931	3	US-08-624-655A-2
21	631	15.0	1052	4	US-08-778-570B-14
22	631	15.0	1052	4	US-09-059-584-14
23	631	15.0	1070	3	US-08-613-009A-11
24	631	15.0	1070	4	US-08-778-570B-13
25	631	15.0	1070	4	US-09-059-584-13
26	629.5	15.0	1053	3	US-08-613-009A-8
27	629.5	15.0	1053	4	US-08-778-570B-10

28	629.5	15.0	1053	4	US-09-059-584-10	Sequence 10, Appl
29	629.5	15.0	1074	3	US-08-613-009A-7	Sequence 7, Appl
30	629.5	15.0	1074	4	US-08-778-570B-9	Sequence 9, Appl
31	629.5	15.0	1074	4	US-09-059-584-9	Sequence 9, Appl
32	625.5	14.9	1076	2	US-08-867-941-19	Sequence 19, Appl
33	625.5	14.9	1076	3	US-09-074-658-19	Sequence 19, Appl
34	606	14.4	930	4	US-08-753-750B-2	Sequence 2, Appl
35	597.5	14.2	911	1	US-08-487-890A-107	Sequence 107, App
36	597.5	14.2	911	2	US-08-478-435-107	Sequence 107, App
37	597.5	14.2	911	2	US-08-337-483-107	Sequence 107, App
38	597.5	14.2	911	2	US-08-478-373-107	Sequence 107, App
39	597.5	14.2	911	3	US-08-474-671-107	Sequence 107, App
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41	597.5	14.2	911	3	US-08-897-438-107	Sequence 107, App
42	597.5	14.2	911	3	US-08-637-654-107	Sequence 107, App
43	597.5	14.2	911	3	US-08-649-518-107	Sequence 107, App
44	590	14.0	914	1	US-08-487-890A-11	Sequence 11, Appl
45	590	14.0	914	2	US-08-478-435-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-817-707-8  
; Sequence 8, Application US/08817707  
; Patent No. 6277382  
; GENERAL INFORMATION:  
; APPLICANT: Stojiljkovic, Igor  
; APPLICANT: So, Magdalene  
; APPLICANT: Hwa, Vivian  
; APPLICANT: Heffron, Fred  
; APPLICANT: Nassif, Xavier  
; TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,707  
; FILING DATE: 19-AUG-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6277382nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 94,784-J  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 790 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-817-707-8

Query Match 99.7% Score 4187; DB 3; Length 790;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 786; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKPLHMLPIAALVGSIFGNPVLAADEAATTTPKAEIKVVRVKDQNPATVERVNLGR 60  
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Best Local Similarity 23.8%; Pred. No. 6.9e-54;  
Matches 248; Conservative 141; Mismatches 317; Indels 338; Gaps 30;

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QY 92 AVRGEVGRVGVSDGV-----SLPDSSENSLVARYGNFNSRLSDPELVRIEIAKAD 147  
DB 103 AVRGVDENRVGWDLGRQAETLSGQPKELPEGVGNFNNTNSIEIENKVTATITKAGD 162  
QY 148 SFNTSGALGGVGVYQTLQHDLLDDROFGVMKNGYSSRNREWTNTLGFVGNDRVDA 207  
DB 163 SLKSGSGLGGSVIPETKDARDYLI-DKDYLSYKRGYQTMNQNLKTLTLAGRSCKFDI 221  
QY 208 ALLYSORRHETESAGERYPEVAGSGAIIGSSRGIPDPKSKHKYHNFGLKIAQINDK 267  
DB 222 LVVDTKRDGHETIENDYKTYPNKQADLSAV--GPTREKADPYQITRQSTLIKLGFPQEN 279  
QY 268 HRIGP-----SFGQQGHNTYIEESYNLTASSWREADDVNRNRNANLFEY- 312  
DB 280 HRLSVALDSTLETGMDLSYIFNQCKNTKCEKY-----GERVINDQSKRKNIOFSYEN 334  
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DB 455 YNVERNITIKELNGKYYGEISLKABGNYGLTOVESAKFLPKSHGYSTDFVNDRLNT 514  
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QY 419 TWSSTQH-----PVKTTNGFSLSDIOIOWNDVFSRADIR 453  
DB 575 GTPVEHTPAPHSAYRCSLMSNKGKOTYLIPVTTKNNVLYFGDNVQLTSLWGLDLN 634  
QY 454 YDHTKMTPELNAECHACDKTPAAN-----TY-- 481  
DB 635 YDHVKYLP-----SYDNKIPVNPGLITGLFKFSSKEYVYVGSYIPPGYENCTYD 686  
QY 482 -----KGWSGVGLAQLNOAHVGYDI-----TSGYRVNASEVYFTYN 521  
DB 687 PCYKKNFEDNALLRLKTDYKHSYNLGLNLDPTNWLRYQLKANGFRAPTSDEIYMTPK 746  
QY 522 HSGNWLNPNIKAERSTHTLSLQGRSEKGLDANLYONNRYNRLSEBQKLTTSQDVGC 581  
DB 747 HPQFSIQPNTDLKAETSKTEVAFTPKNSYITLNAFQNDYRNFID-----LVEVGE 799  
QY 582 TQNNYYGMCNPSY-----KPEWQONIDKARIGLELTGLNVTYKASVFPBGKLF 636  
DB 800 -----RPIEGSAIKYPPHONQNRDRVRVRIEIASRLEMGDLFEKL-QGFHLG 847  
QY 637 GSLGYAKSKLSDGNSL-----LSTQPKPIAGVDYES 668  
DB 848 YKFTYQKGRK-DNGLHPKYKEFLELNKDEHPEYEAIRKQPMNALQTTSTVYNIYDA 906  
QY 669 PSEKGVFRLTLVLGAKAADA-----QYT-----VVENKGRGTPPKQKVK 709  
DB 907 PSQKGVDMYIITNVAAKAKADSPNSQWTSWVARKQYTDNATIDPATKANG-----KQVK 962  
QY 710 DYP--WLNKSAVYFDMYGVFKLAKNLTLAGVYVNVENRYTWTWDSLRGLYSSTTNAVD 767  
DB 963 DSRGLRNRYTYDITAYWPKIKNLTFTAGVYVNLTKKYLWDSARSVRHLGTINRVKT 1022  
QY 768 D-GKGLDRYASGRNVAVSLDMKF 790

DB 1023 ETGEGLNRFYAPGRNRYRMSVQFEF 1046  
RESULT 8  
ABP77288  
ID ABP77288 standard; protein; 809 AA.  
XX  
AC ABP77288;  
DT 07-MAR-2003 (first entry)  
XX  
DE N. gonorrhoeae amino acid sequence SEQ ID 1106.  
XX  
KW Antibacterial; infection; vaccine; gene therapy.  
XX  
OS Neisseria gonorrhoeae.  
XX  
PN WO200279243-A2.  
XX  
XX 10-OCT-2002.  
XX  
PF 12-FEB-2002; 2002WO-IB002069.  
XX  
PR 12-FEB-2001; 2001GB-00003424.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
PI Fontana MR, Pizza M, Masignani V, Monaci E;  
XX  
DR WPI; 2003-058415/05.  
DR N-PSDB; ABZ38258.  
XX  
PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
medicament for treating or preventing N. gonorrhoeae infection.  
XX  
PS Disclosure; Page 268; 815pp; English.  
XX  
CC The present invention relates to proteins from Neisseria gonorrhoeae.  
CC Also disclosed are the nucleic acid molecules encoding the proteins and  
antibodies that specifically bind to the proteins. The composition  
comprising the protein, nucleic acid or antibody is useful for the  
manufacture of a medicament for treating or preventing N. gonorrhoeae  
infection, this may be in the form of a vaccine or gene therapy.  
CC  
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid  
molecules of the invention  
XX  
XX Sequence 809 AA;  
Query Match 18.0%; Score 755; DB 6; Length 809;  
Best Local Similarity 26.5%; Pred. No. 1.2e-53;  
Matches 231; Conservative 153; Mismatches 341; Indels 146; Gaps 31;  
QY 3 PUHMLPIAALVGSIFGNPVLAADEAATETTPKAB-IKEVRV-----KQOLNAPATVERVN 57  
DB 2 PIPFPLVAAAIAQAQAFAPADPA-----PQSAQTLNEITVTGHTKQKLGEEKIRKT 56  
QY 58 LGRIQOEMIRONKDLVRYSTDVGLSDSGR-HQKGFVAVGVEGNRVGVSDVGLSDPSEEN 116  
DB 57 LDKL---LANDEHGLVRYDPGISVVEGGRAGSNGFTIRGVDKDRVAINVDGLAQAESRS 113  
QY 117 ---SLYARYGNFNSRLSDPELVRIEIAKADSFNTGSGALGGGVYQTLQGHDL 172  
DB 114 EAFQLFGAYGNFANRNTSEPESEVITTKGADSLKSGSALGAVNYQTKASDYVS 173  
QY 173 DDQFGVMKNGYSSRNREWTNTL-----FGVSNDRVDAALLYSORRHETESAGERY 227  
DB 174 EKPVHLGIGKSGVGKNSQKTFSSITAAAGRLFG-----LDALLVYTRRFKGTNRSTEG- 227  
QY 228 PVEGAGSGNAI-----RGSRRGIPDPSKHKYHNFGLKIAQINDKHRIGP 272  
DB 228 DVEIKNDGVDFDPAFPSRSLTYKATGVARSQDPQEWNVKSTLTKGYNFNRNRIGW 287

comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy.

Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention

CC comprising the protein, nucleic acid or antibody is useful for the  
CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
CC infection, this may be in the form of a vaccine or gene therapy.  
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid  
CC molecules of the invention  
XX  
SQ Sequence 288 AA;

Query Match 34.8%; Score 1462.5; DB 6; Length 288;  
Best Local Similarity 95.5%; Pred. No. 1.2e-113;  
Matches 274; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 391 LSLTFASRRREFENLDRDYFSSRVSTSSIQHPVKTTNGFSLSDQIOWNDVFSRA 450  
Db 1 LSFKTFASRRREFENLDRDYFSSQISRTSSIQHPVKTTNGFSLSDQIOWNDVFSRA 60

Qy 451 DIRYDHTKMTPOELNAEACHADKTPPAANTYKMGSGFVGLAAQLNQAWHVGYDITSGYRV 510  
Db 61 DIRYDHTKMTPOELNAEACHADKTPPAANTYKMGSGFVGLAAQLNQAWHVGYDITSGYRV 120

Qy 511 PNASEVFTYNGSGNWLPNLNAERSTHTLSLQGRSEKGTLDANLYQNNYRNFLEE 570  
Db 121 PNASEVFTYNGSGNWLPNLNAERSTHTLSLQGRSEKGTLDANLYQNNYRNFLEE 180

Qy 571 QKLTSGDVGCTQNNYYGMCNPSYSEKPEWQONIDKARIRGLELTGRNLNVTKVASFVP 630  
Db 181 QKLTSGDVGCTQNNYYGMCNPSYSEKPEWQONIDKARIRGLELTGRNLNVTKVASFVP 240

Qy 631 EGWKLFGSLGYAKSKLSDGNSLLSTQPPKVIAGVDYESPEKNGVFS 677  
Db 241 EGWKLFGSLGYAKSKLSDGNSLLSTQPPKVIAGVDYEARA-KNGVCS 286

RESULT 6  
ABP77003  
ID ABP77003 standard; protein; 284 AA.

AC ABP77003;  
XX  
XX  
DT 07-MAR-2003 (first entry)  
XX  
DE N. gonorrhoeae amino acid sequence SEQ ID 536.  
XX  
KW Antibacterial; infection; vaccine; gene therapy.  
XX  
OS Neisseria gonorrhoeae.

XX WO200279243-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 12-FEB-2002; 2002WO-IB002069.  
XX  
XX 12-FEB-2001; 2001GB-00003424.  
XX  
XX (CHIR-) CHIRON SPA.

XX Fontana MR, Pizza M, Massignani V, Monaci E;  
XX WPI; 2003-058415/05.  
XX N-PSDB; ABZ37973.  
XX

PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
PT medicament for treating or preventing N. gonorrhoeae infection.

XX Disclosure; Page 227; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.  
XX Also disclosed are the nucleic acid molecules encoding the proteins and  
XX antibodies that specifically bind to the proteins. The composition  
XX comprising the protein, nucleic acid or antibody is useful for the  
XX manufacture of a medicament for treating or preventing N. gonorrhoeae  
XX infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid  
CC molecules of the invention  
XX  
SQ Sequence 284 AA;

Query Match 34.4%; Score 1445; DB 6; Length 284;  
Best Local Similarity 98.6%; Pred. No. 3.5e-112;  
Matches 280; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKABIKVVRVKDQLNAPATVERVNLGR 60  
Db 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKABIKVVRVKDQLNAPATVERVNLDR 60

Qy 61 IQEMIEDNKDLVRYSTDVGLSDSGRHKQGFVARGVGEVGVSDIGVSLPDSSENSIYA 120  
Db 61 IQEMIEDNKDLVRYSTDVGLSDSGRHKQGFVARGVGEVGVSDIGVSLPDSSENSIYA 120

Qy 121 RYGNFNSRLSIDPELVNIEIAKADSFNTGSGALGGVNYQTLQGHDLILLDDRQFGVM 180  
Db 121 RYGNFNSRLSIDPELVNIEIAKADSFNTGSGALGGVNYQTLQGHDLILLDDRQFGVM 180

Qy 181 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSQRRGHETESAGRGYPVREGAGSGAIRG 240  
Db 181 MKNGYSSRNREWTNTLFGVSNDRVDAALLYSQRRGHETESAGRGYPVREGAGSGANIRG 240

Qy 241 SSRGIPDPSPKHVHNFGLKIAYQINDKHRIQINDKHRIQINDKHRIQINDKHRIQINDKHRI 284  
Db 241 SARGIPDPSPKHVHNFGLKIAYQINDKHRIQINDKHRIQINDKHRIQINDKHRIQINDKHRI 284

RESULT 7  
ADT05707  
ID ADT05707 standard; protein; 1046 AA.

AC ADT05707;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
DE Haemophilus influenzae (NTHi) protein - SEQ ID 743.  
XX  
KW middle ear bacterial infection; nasopharynx bacterial infection.  
XX  
OS Haemophilus influenzae.  
XX  
XX WO2004078949-A2.  
XX  
XX 16-SEP-2004.  
XX  
XX 05-MAR-2004; 2004WO-US007001.  
XX  
XX 06-MAR-2003; 2003US-0453134P.  
XX  
XX (CHIL-) CHILDRENS HOSPITAL INC.  
XX  
XX Bakaletz LO, Munson RS, Dyer DW;  
XX WPI; 2004-662422/64.  
XX N-PSDB; ADT05706.

PT New polynucleotides of nontypeable strain of Haemophilus influenzae,  
PT useful for treating or preventing NTHi bacterial infections of the middle  
PT ear and/or nasopharynx.

XX Claim 3; SEQ ID NO 743; 88pp; English.

XX The invention comprises nucleotide sequences (genes) from the genome of a  
XX nontypeable strain of Haemophilus influenzae (NTHi). The NTHi DNA  
XX sequences of the invention are useful for treating or preventing NTHi  
XX bacterial infections of the middle ear and/or nasopharynx. The present  
XX amino acid sequence represents an NTHi protein of the invention.  
XX  
SQ Sequence 1046 AA;



XX AAR95566;  
 AC 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 28-AUG-1996 (first entry)  
 DE N. meningitidis serotype A haemoglobin receptor.  
 XX Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; meningitis.  
 KW Neisseria meningitidis serogroup A.  
 OS WO9612020-A2.  
 PN 25-APR-1996.  
 XX 17-OCT-1995; 95WO-US013623.  
 XX 18-OCT-1994; 94US-00326670.  
 PR 02-OCT-1995; 95US-00537361.  
 XX (UYOR-) UNIV OREGON HEALTH SCI.  
 PA Stojiljkovic I, So M, Hwa V, Heffron F, Nassif X;  
 XX WPI: 1996-222006/22.  
 DR N-PSDB; AAT26998.  
 XX DNA encoding Neisseria haemoglobin receptor proteins - for use in  
 PT preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.  
 XX Claim 3; Page 55-58; 104pp; English.  
 CC A bacterial haemoglobin receptor (AAR95566) was identified as the product  
 CC of the hmbR gene (AAR26998) of N. meningitidis serotype A. The  
 CC haemoglobin receptor is thought to be involved in hemin utilisation by  
 CC the bacterium. This dependence on host iron stores is a potential route  
 CC for therapeutic intervention strategies. The receptor can be expressed in  
 CC transformed hosts, e.g. attenuated Salmonella cells. It is useful as a  
 CC vaccine for meningitis, or can be used to raise antibodies of diagnostic  
 CC appln. Similar receptor proteins were obtd. from N. meningitidis  
 CC serotypes B (AAR95567) and C (AAR95565) from N. gonorrhoeae (AAR95568).  
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to  
 CC correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)  
 XX Sequence 791 AA;  
 SQ

Query Match 87.3%; Score 3665.5; DB 2; Length 791;  
 Best Local Similarity 86.9%; Pred. No. 1.5e-297;  
 Matches 687; Conservative 44; Mismatches 59; Indels 1; Gaps 1;  
 QY 1 MKPLHMLPTAALVGSIFGNPVLAADEAATETTPVKAIEKVRVKDQINAPATVVRNLCR 60  
 DB 1 MKPLQMPPTAALIGSIFGNPVLAADEAATETTPVKAIEKVRVKDQINAPATVVRNLCR 60  
 QY 61 IQQEMIRDNKDLVRYSTDTGLSDSGRKHQGFARVGEGRVGVSDIGVSLPDSEENSLYA 120  
 DB 61 IQQEMIRDNKDLVRYSTDTGLSDSGRKHQGFARVGEGRVGVSDIGVSLPDSEENSLYA 120  
 QY 121 RYGNFNSRLSIDPELVRIETIAKAGDSFNTGSGALGGGVNYQTLQGHDLILLDDROFGVM 180  
 DB 121 RYGNFNSRLSIDPELVRIETIAKAGDSFNTGSGALGGGVNYQTLQGHDLILLDDROFGVM 180  
 QY 181 MKNGYSRNRWNTTLFGVSNDRVDAALLYSQRRGHETESAGERGYVPEGAGSGAIIRG 240  
 DB 181 MKNGYSRNRWNTTLFGVSNDRVDAALLYSQRRGHETESAGERGYVPEGAGSGANIRG 240  
 QY 241 SSRGIDPPSKKHNFILGKIAYQINDKHRIKRPSPNGQOQHNYTIEESYNLTASSWREDD 300  
 DB 241 SARGIDPPSKKHNFILGKIAYQINDKHRIKRPSPNGQOQHNYTIEESYNLTASSWREDD 300  
 QY 301 VNRNRNANLFYEWTSPDSNMLSSLKADFVYQTTKVAAVNNKGSFPTDYSTWTRNYNQKDL 360

DB 301 VNRNRNANLFYEWTSPDSNMLSSLKADFVYQTTKVAAVNNKGSFPTDYSTWTRNYNQKDL 360  
 QY 361 NIYNRSMOTRFRFTLRMDSQLQ-L-GGQHRSLKTEFASREFFENLRDDYFSEVSRVT 419  
 DB 361 EYINRSMOTRFRFTLRMDSQLQ-L-GGQHRSLKTEFASREFFENLRDDYFSEVSRVT 420  
 QY 420 TSSIQHPVKTTNYGFSLSDOIQWMDVFSRADIRYDHTKMTQELNAEACHADCKTPPAAN 479  
 DB 421 TNSIQHPVKTTNYGFSLSDOIQWMDVFSRADIRYDHTKMTQELNAEACHADCKTPPAAN 480  
 QY 480 TYKWSGFGVGLAAQLNQAHVGYDITSGYRVNASEVYTYNHGSGNWLPNPNLKAERST 539  
 DB 481 TYKWSGFGVGLAAQLNQAHVGYDITSGYRVNASEVYTYNHGSGNWLPNPNLKAERST 540  
 QY 540 THTLSIQSESEKGTLDANLYQNNYRNFSEEQKLTSGDVGCTQNNYVYGMCSNPYSEK 599  
 DB 541 THTLSIQSESEKGTLDANLYQNNYRNFSEEQKLTSGDVGCTQNNYVYGMCSNPYSEK 600  
 QY 600 EWMQONIDKARIRGLELTGRLNVTKVASFVPSGKWLFGSLGYAKSKLSDNSLLSTQPPK 659  
 DB 601 DMQKNIDKARIRGLELTGRLNVTKVASFVPSGKWLFGSLGYAKSKLSDNSLLSTQPLK 660  
 QY 660 VIAGVDYSPSEKSGVFSRLTYLGAKKADQYTYVYENKRGRTPLQKKYKDYPLNKSAY 719  
 DB 661 VIAGVDYSPSEKSGVFSRLTYLGAKKADQYTYVYENKRGRTPLQKKYKDYPLNKSAY 720  
 QY 720 VEDMYGFYKLNLTIRAGVYVFNKRYTTWDSLGLYSYSTNAVDKGLDRVRASG 779  
 DB 721 VEDMYGFYKLNLTIRAGVYVFNKRYTTWDSLGLYSYSTNAVDKGLDRVRASG 780  
 QY 780 RNYAVSLDWKF 790  
 DB 781 RNYAVSLEWKF 791

RESULT 5  
 ABP76983  
 ID ABP76983 standard; protein; 288 AA.  
 XX AC ABP76983;  
 XX 07-MAR-2003 (first entry)  
 DT N. gonorrhoeae amino acid sequence SEQ ID 496.  
 DE Antibacterial; infection; vaccine; gene therapy.  
 XX OS Neisseria gonorrhoeae.  
 XX WO200279243-A2.  
 XX 10-OCT-2002.  
 XX 12-FEB-2002; 2002WO-IB002069.  
 XX 12-FEB-2001; 2001GB-00003424.  
 XX (CHIR-) CHIRON SPA.  
 PA Fontana MR, Pizza M, Masignani V, Monaci E;  
 PI WPI: 2003-058415/05.  
 DR N-PSDB; ABZ37953.  
 XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
 XX medicament for treating or preventing N. gonorrhoeae infection.  
 XX Disclosure; Page 224; 815pp; English.  
 CC The present invention relates to proteins from Neisseria gonorrhoeae.  
 CC Also disclosed are the nucleic acid molecules encoding the proteins and  
 CC antibodies that specifically bind to the proteins. The composition

QY 420 TSSIQHPVKTNYGSLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAAN 479  
 Db 420 TSSIQHPVKTNYGSLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAAN 479  
 QY 480 TYKHSFGVGLAAQLNQAHVGYDITSGYRVPNASEVFTYHNHSGNWLPPNPKAERST 539  
 Db 480 TYKHSFGVGLAAQLNQAHVGYDITSGYRVPNASEVFTYHNHSGNWLPPNPKAERST 539  
 QY 540 THTLSLQGRSEKGTLDANLYQNNYENFLSEBQKLTSGDVCTOMNYYYGWCSPYSEKP 599  
 Db 540 THTLSLQGRSEKGTLDANLYQNNYENFLSEBQKLTSGDVCTOMNYYYGWCSPYSEKP 599  
 QY 600 EQWQONIDKARIRGLIELTGRNLNVTVKASVPEGWKLFGLSLGYAKSKLSDGNSLLSTQPPK 659  
 Db 600 EQWQONIDKARIRGLIELTGRNLNVTVKASVPEGWKLFGLSLGYAKSKLSDGNSLLSTQPPK 659  
 QY 660 VIAGVDYSPSEKMGVFSRLTYLGAKKAKDAQYTYVENKGRGTPLOKKVKDYPMLNKSAY 719  
 Db 660 VIAGVDYSPSEKMGVFSRLTYLGAKKAKDAQYTYVENKGRGTPLOKKVKDYPMLNKSAY 719  
 QY 720 VEDMGVFKLAKNLTLAGVNVNENKYYTWDLSRLGLYSYSTTNAVDKGLDRYRAG 779  
 Db 720 VEDMGVFKLAKNLTLAGVNVNENKYYTWDLSRLGLYSYSTTNAVDKGLDRYRAG 779  
 QY 780 RNYAVSLDWKF 790  
 Db 780 RNYAVSLEWKF 790

## RESULT 3

AAR95567  
 ID AAR95567 standard; protein; 792 AA.

AC AAR95567;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-AUG-1996 (first entry)

DE N. meningitidis serotype B haemoglobin receptor.

XX Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; meningitis.

XX Neisseria meningitidis serogroup B.

XX W09612020-A2.

XX 25-APR-1996.

XX 17-OCT-1995; 95WO-US013623.

XX 18-OCT-1994; 94US-00326670.

XX 02-OCT-1995; 95US-00537361.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Stojiljkovic I, So M, Hwa V, Heffron F, Nassif X;

XX WPI; 1996-222006/22.

XX N-PSDB; AAT26999.

XX DNA encoding Neisseria haemoglobin receptor proteins - for use in preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.

XX Claim 4; Page 58-61; 104pp; English.

XX A bacterial haemoglobin receptor (AAR95567) was identified as the product of the hmbR gene (AAT26999) of N. meningitidis serotype B. The haemoglobin receptor is thought to be involved in hemin utilisation by the bacterium. This dependence on host iron stores is a potential route for therapeutic intervention strategies. The receptor can be expressed in transformed hosts, e.g. attenuated Salmonella cells. It is useful as a

CC vaccine for meningitis, or can be used to raise antibodies of diagnostic appln. Similar receptor proteins were obtd. from N. meningitidis CC serotypes A (AAR95566) and C (AAR95565) and from N. gonorrhoeae CC (AAR95568). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

SQ Sequence 792 AA;

Query Match 90.8%; Score 3812; DB 2; Length 792;

Best Local Similarity 91.2%; Pred. No. 8e-310;

Matches 722; Conservative 25; Mismatches 43; Indels 2; Gaps 2;

QY 1 MKPLHMLPIAALVGSIFGNPVLADEAATETTPVKAETKEVRVKDQLNAPATVERVNLGR 60  
 Db 1 MKPLHMLPIAALVGSIFGNPVLADEAATETTPVKAETKEVRVKDQLNAPATVERVNLGR 60  
 QY 61 IQQEMIRNDKOLVRYSTDVGLSDSGRHQKQFAVRGVEGNRVGVSIDGVSLLPSEENSLYA 120  
 Db 61 IQQEMIRNDKOLVRYSTDVGLSDSGRHQKQFAVRGVEGNRVGVSIDGVSLLPSEENSLYA 120  
 QY 121 RYGFNSRLSIDPELVNIEIAKADSFNTGSGALGGGVNYQTLOGHDLILLDDRFQGM 180  
 Db 121 RYGFNSRLSIDPELVNIEIAKADSFNTGSGALGGGVNYQTLOGHDLILLDDRFQGM 180  
 QY 181 MKNGYSSRNREWTNTLGFVSNDRVDAAALYSQRRGHETESAGERYPVEGAGSGAIIRG 240  
 Db 181 MKNGYSSRNREWTNTLGFVSNDRVDAAALYSQRRGHETESAGERYPVEGAGSGAIIRG 240  
 QY 241 SSRGIPDPSPKHYNFLGKIAYQINDKRIHIGPSFNGQQGHNYTIEESYNLTASSWREADD 300  
 Db 241 SARGIPDPSPKHYSFLGKIAYQINDKRIHIGPSFNGQQGHNYTIEESYNLTASSWREADD 300  
 QY 301 VNRERNANLFYEWTDPDSNWLSSLKADFDYQTKVAANVKNKGFPP-TDYSTWTRNNQKDL 359  
 Db 301 VNRERNANLFYEWTDPDSNWLSSLKADFDYQTKVAANVKNKGFPP-TDYSTWTRNNQKDL 359  
 QY 360 ENIYNRSMDFRKFRTLRMDSQPLQ-L-GQHRLSLKTFASSRREFENLRDDYFYSERVSR 418  
 Db 360 DEIYNRSMDFRKFRTLRMDSQPLQ-L-GQHRLSLKTFASSRREFENLRDDYFYSERVSR 418  
 QY 419 TTSSIQHPVKTNYGSLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAA 478  
 Db 419 TTSSIQHPVKTNYGSLSDQIQWNVDFSSRADIRYDHTKMTPOELNAEACHADCKTPPAA 478  
 QY 479 NTYKHSFGVGLAAQLNQAHVGYDITSGYRVPNASEVFTYHNHSGNWLPPNPKAERST 538  
 Db 479 NTYKHSFGVGLAAQLNQAHVGYDITSGYRVPNASEVFTYHNHSGNWLPPNPKAERST 538  
 QY 539 THTLSLQGRSEKGTLDANLYQNNYENFLSEBQKLTSGDVCTOMNYYYGWCSPYSEK 598  
 Db 539 THTLSLQGRSEKGTLDANLYQNNYENFLSEBQKLTSGDVCTOMNYYYGWCSPYSEK 598  
 QY 599 PEWQONIDKARIRGLIELTGRNLNVTVKASVPEGWKLFGLSLGYAKSKLSDGNSLLSTQPP 658  
 Db 599 PEWQONIDKARIRGLIELTGRNLNVTVKASVPEGWKLFGLSLGYAKSKLSDGNSLLSTQPP 658  
 QY 659 KVIAGVDYSPSEKMGVFSRLTYLGAKKAKDAQYTYVENKGRGTPLOKKVKDYPMLNKSAY 718  
 Db 659 KVIAGVDYSPSEKMGVFSRLTYLGAKKAKDAQYTYVENKGRGTPLOKKVKDYPMLNKSAY 718  
 QY 719 YVPDMYGFYKLVKLNLTLAGVNVNENKYYTWDLSRLGLYSYSTTNAVDKGLDRYRAG 778  
 Db 719 YVPDMYGFYKLVKLNLTLAGVNVNENKYYTWDLSRLGLYSYSTTNAVDKGLDRYRAG 778  
 QY 779 GRNYAVSLDWKF 790  
 Db 779 GRNYAVSLDWKF 790  
 QY 781 SRNYAVSLEWKF 792  
 Db 781 SRNYAVSLEWKF 792

## RESULT 4

AAR95566

ID AAR95566 standard; protein; 791 AA.

```
XX SQ Sequence 790 AA;
Query Match 100.0%; Score 4200; DB 2; Length 790;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 790; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKEVRVKQQLNAPATVERVNLGR 60
DB 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKEVRVKQQLNAPATVERVNLGR 60

QY 61 IQQEMIRNDKLVRYSTDVGLSDSGRHOKGFAVRGVEGNRVGVSIDGVSPLDSEENSLYA 120
DB 61 IQQEMIRNDKLVRYSTDVGLSDSGRHOKGFAVRGVEGNRVGVSIDGVSPLDSEENSLYA 120

QY 121 RYGNFNSSRLSIDPELVNRIETAKGDSFNTGSGALGGGVNYQTQGHDLILLDDRRQFGVM 180
DB 121 RYGNFNSSRLSIDPELVNRIETAKGDSFNTGSGALGGGVNYQTQGHDLILLDDRRQFGVM 180

QY 181 MKNGYSSRNREWTNTLGFVSNDRVDAALLYQRRGHETESAGERGYPEVGAGSGAIIIRG 240
DB 181 MKNGYSSRNREWTNTLGFVSNDRVDAALLYQRRGHETESAGERGYPEVGAGSGAIIIRG 240

QY 241 SSRGIPDPSKHKYHNFGLGKIAYQINDKHRIGPSFNGQQGHNTTIESYNTLTASSWREADD 300
DB 241 SSRGIPDPSKHKYHNFGLGKIAYQINDKHRIGPSFNGQQGHNTTIESYNTLTASSWREADD 300

QY 301 VNRRENANLFYEWTPDPSNWLSSLKADFDYQTTKVAAVNNKGSFPPTDYSTWTNRYNOKOLE 360
DB 301 VNRRENANLFYEWTPDPSNWLSSLKADFDYQTTKVAAVNNKGSFPPTDYSTWTNRYNOKOLE 360

QY 361 NIYNRSMDTRFKRFTLRDMSQPLQGGQHRLSLKTFFASRRREFENLRDDYFESRVSRTT 420
DB 361 NIYNRSMDTRFKRFTLRDMSQPLQGGQHRLSLKTFFASRRREFENLRDDYFESRVSRTT 420

QY 421 SSIQHPVKTNTYGFSLSDQIQWNVFSSRADIRYDHTKMTPOELNAEACHACDKTTPAANT 480
DB 421 SSIQHPVKTNTYGFSLSDQIQWNVFSSRADIRYDHTKMTPOELNAEACHACDKTTPAANT 480

QY 481 YKMGSGFVGLAQLAQWAMHVGDIYSGYRVPNASEVYFTYNGSGNWLNPENLKAERSTT 540
DB 481 YKMGSGFVGLAQLAQWAMHVGDIYSGYRVPNASEVYFTYNGSGNWLNPENLKAERSTT 540

QY 541 HTLSLQGRSEKGTLDANLYQNNYRNFLEBEOKLITSGDVGCTOMNYYYGMCNPNYSEKPE 600
DB 541 HTLSLQGRSEKGTLDANLYQNNYRNFLEBEOKLITSGDVGCTOMNYYYGMCNPNYSEKPE 600

QY 601 WQWQNDKARIRGLEITGRNLNTKVASFVPEGWKLFGLSGLYAKSKLSGDSNLSLSTQPPKV 660
DB 601 WQWQNDKARIRGLEITGRNLNTKVASFVPEGWKLFGLSGLYAKSKLSGDSNLSLSTQPPKV 660

QY 661 IAGVDYESPEKGVFSRLTYLGAKAKADAQYTVYENKRGRTFLOKKVDYFWLNKSAIV 720
DB 661 IAGVDYESPEKGVFSRLTYLGAKAKADAQYTVYENKRGRTFLOKKVDYFWLNKSAIV 720

QY 721 FDMYGFYKLAKNLTLAGYVYFNRYKTYTWDLSRLGLYSYTTNAVDRDCKGLDRYRASGR 780
DB 721 FDMYGFYKLAKNLTLAGYVYFNRYKTYTWDLSRLGLYSYTTNAVDRDCKGLDRYRASGR 780

QY 781 NYAVSLDWKF 790
DB 781 NYAVSLDWKF 790
```

## RESULT 2

AAR95565  
ID AAR95565 standard; protein; 790 AA.

XX  
AC AAR95565;

XX 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 28-AUG-1996 (first entry)

```
XX N. meningitidis serotype C haemoglobin receptor.
XX Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; meningitis.
XX Neisseria meningitidis serogroup C.
XX WO9612020-A2.
XX 25-APR-1996.
XX 17-OCT-1995; 95WO-US013623.
XX 18-OCT-1994; 94US-00326670.
XX 02-OCT-1995; 95US-00537361.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Stojiljkovic I, So M, Hwa V, Heffron F, Nassif X;
XX WPI: 1996-222006/22.
XX N-PSDB; AAT26997.
XX DNA encoding Neisseria haemoglobin receptor proteins - for use in
XX preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.
XX Claim 2; Page 50-52; 104pp; English.
XX A bacterial haemoglobin receptor (AAR95565) was identified as the product
XX of the hmbR gene (AAR26997) of N. meningitidis serotype C isolate 8013
XX clone 6. The haemoglobin receptor is thought to be involved in hemin
XX utilisation by the bacterium. This dependence on host iron stores is a
XX potential route for therapeutic intervention strategies. The receptor can
XX be expressed in transformed hosts, e.g. attenuated Salmonella cells. It
XX is useful as a vaccine for meningitis, or can be used to raise antibodies
XX of diagnostic appln. Similar receptor proteins were obt'd. from N.
XX meningitidis serotypes A and B and from N. gonorrhoeae (see also AAR95566
XX -68). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
XX 2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 790 AA;
Query Match 90.8%; Score 3814; DB 2; Length 790;
Best Local Similarity 91.0%; Pred. No. 5.4e-310;
Matches 720; Conservative 25; Mismatches 44; Indels 2; Gaps 2;

QY 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKEVRVKQQLNAPATVERVNLGR 60
DB 1 MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAIEKEVRVKQQLNAPATVERVNLGR 60

QY 61 IQQEMIRNDKLVRYSTDVGLSDSGRHOKGFAVRGVEGNRVGVSIDGVSPLDSEENSLYA 120
DB 61 IQQEMIRNDKLVRYSTDVGLSDSGRHOKGFAVRGVEGNRVGVSIDGVSPLDSEENSLYA 120

QY 121 RYGNFNSSRLSIDPELVNRIETAKGDSFNTGSGALGGGVNYQTQGHDLILLDDRRQFGVM 180
DB 121 RYGNFNSSRLSIDPELVNRIETAKGDSFNTGSGALGGGVNYQTQGHDLILLDDRRQFGVM 180

QY 181 MKNGYSSRNREWTNTLGFVSNDRVDAALLYQRRGHETESAGERGYPEVGAGSGAIIIRG 240
DB 181 MKNGYSSRNREWTNTLGFVSNDRVDAALLYQRRGHETESAGERGYPEVGAGSGAIIIRG 240

QY 241 SSRGIPDPSKHKYHNFGLGKIAYQINDKHRIGPSFNGQQGHNTTIESYNTLTASSWREADD 300
DB 241 SSRGIPDPSKHKYHNFGLGKIAYQINDKHRIGPSFNGQQGHNTTIESYNTLTASSWREADD 300

QY 301 VNRRENANLFYEWTPDPSNWLSSLKADFDYQTTKVAAVNNKGSFPPTDYSTWTNRYNOKOLE 360
DB 301 VNRRENANLFYEWTPDPSNWLSSLKADFDYQTTKVAAI-NKGSFPPTNYTWTETXHKKEVG 359

QY 361 NIYNRSMDTRFKRFTLRDMSQPLQ-L-GGOHRLSLKTFFASRRREFENLRDDYFESRVSRT 419
DB 360 EIYNRSMDTRFKRFTLRDMSQPLQ-LGGGRHRLSFKTFFASRRREFENLRDDYFESRVSRT 419
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 6, 2005, 14:49:54 ; Search time 168 Seconds  
(without alignments)  
1818.695 Million cell updates/sec

Title: US-09-665-358-8

Perfect score: 4200

Sequence: 1 MKPLHMLPTAALVGSIFGNP.....GLDRYASGRNVAVSLDWKF 790

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4200	100.0	790	2	AAR95568 N. gonorr
2	3814	90.8	790	2	AAR95565 N. mening
3	3812	90.8	792	2	AAR95567 N. mening
4	3655.5	87.3	791	2	AAR95566 N. mening
5	1462.5	34.8	288	6	ABP76983 N. gonorr
6	1445	34.4	284	6	ABP77003 N. gonorr
7	760	18.1	1046	8	ADT05707 Haemophil
8	755	18.0	809	6	ABP77288 N. gonorr
9	753.5	17.9	967	3	AAB44536 Virulence
10	753.5	17.9	967	5	ABP54488 Pasteurel
11	737.5	17.6	669	3	AAB44565 Virulence
12	737.5	17.6	669	5	ABP54517 Pasteurel
13	702.5	16.7	789	7	ABO78265 Pseudomon
14	669.5	15.9	943	5	ABG91056 Neisseria
15	663.5	15.8	1046	8	ADT05701 Haemophil
16	661.5	15.8	943	8	ADP08381 Neisseria
17	649	15.5	698	6	ABU49701 Protein e
18	642.5	15.3	971	3	AAB21223 Haemophil
19	640	15.2	931	2	AAM04867 Transferr
20	631	15.0	1070	2	AAW35314 M. catarr
21	629.5	15.0	1074	2	AAW35312 M. catarr
22	625.5	14.9	1074	2	AAW35381 M. catarr
23	611	14.5	116	6	ABP76975 N. gonorr
24	606	14.4	930	2	AAW18061 Pasteurel
25	597.5	14.2	911	2	AAR77892 Bacterial

#### ALIGNMENTS

##### RESULT 1

AAR95568  
ID AAR95568 standard; protein; 790 AA.

AC AAR95568;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-AUG-1996 (first entry)

XX N. gonorrhoeae B haemoglobin receptor.

DE Bacterial haemoglobin receptor; hmbR gene; antibody; vaccine; gonorrhoea.

XX Neisseria gonorrhoeae.

OS Neisseria gonorrhoeae.

XX WO9612020-A2.

XX 25-APR-1996.

XX 17-OCT-1995; 95WO-US013623.

XX 18-OCT-1994; 94US-00326670.

PR 02-OCT-1995; 95US-00537361.

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XX Stojiljkovic I, So M, Hwa V, Heffron F, Nassif X;

XX WPI; 1996-222006/22.

DR N-PSDB; AAT27000.

XX DNA encoding Neisseria haemoglobin receptor proteins - for use in

PT preparing polypeptide(s) and antibodies for vaccines for e.g. meningitis.

XX Claim 5; Page 67-69; 104pp; English.

XX A bacterial haemoglobin receptor (AAR95568) was identified as the product

CC of the hmbR gene (AAT27000) of N. gonorrhoeae strain MS11A. The

CC haemoglobin receptor is thought to be involved in hemin utilization by

CC the bacterium. This dependence on host iron stores is a potential route

CC for therapeutic intervention strategies. The receptor can be expressed in

CC transformed hosts, e.g. attenuated Salmonella cells. It is useful as a

CC vaccine for gonorrhoea, or can be used to raise antibodies of diagnostic

CC appln. Similar receptor proteins were obtd. from N. meningitidis

CC serotypes A (AAR95566), B (AAR95567) and C (AAR95565). (Updated on 25-MAR

CC -2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)

CC (Updated on 27-AUG-2003 to correct OS field.)

Aaw08966 Amino aci  
Aay51780 H. influe  
Aaw54124 H. influe  
Aay80362 H. influe  
Aaw08963 Amino aci  
Aay51693 H. influe  
Aaw53048 H. influe  
Aay80359 H. influe  
Aay51769 N. mening  
Aay80373 N. mening  
Aar34403 Sequence  
Aay51768 N. mening  
Aay80372 N. mening  
Aar34402 Sequence  
Aaw08961 Amino aci  
Aaw08959 Amino aci  
Aay51689 H. influe  
Aay51691 H. influe  
Aaw53044 H. influe  
Aaw53046 H. influe